

Mon Apr 5 09:54:04 2004

us-10-066-500-9.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:52:57 ; Search time 40 Seconds
(without alignments)
767.445 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGMAVFLASRLGQGLL.....QNVGSLVLTAVIRTVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1070241 seqs, 262374223 residues

Total number of hits satisfying chosen parameters: 1070241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
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16: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	117	10	US-09-946-374-6
2	609	100.0	117	12	US-10-081-056-6
3	609	100.0	117	13	US-10-066-500-9
4	609	100.0	117	14	US-10-002-796-9
5	609	100.0	117	14	US-10-066-273-9
6	609	100.0	117	14	US-10-066-494-9
7	609	100.0	117	14	US-10-066-269-9
8	609	100.0	117	14	US-10-006-856A-6
9	609	100.0	117	14	US-10-066-211-9
10	609	100.0	117	14	US-10-066-193-9
11	609	100.0	117	14	US-10-006-818A-6
12	609	100.0	117	14	US-10-015-933A-6
13	609	100.0	117	14	US-10-015-869A-6
14	609	100.0	117	14	US-10-012-121A-6
15	609	100.0	117	14	US-10-006-116A-6

16	609	100.0	117	14	US-10-006-117A-6
17	609	100.0	117	14	US-10-017-527A-6
18	609	100.0	117	14	US-10-013-913A-6
19	609	100.0	117	14	US-10-007-194A-6
20	609	100.0	117	14	US-10-013-430A-6
21	609	100.0	117	14	US-10-011-671A-6
22	609	100.0	117	14	US-10-012-755A-6
23	609	100.0	117	14	US-10-015-386A-6
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25	609	100.0	117	14	US-10-226-739-9
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28	609	100.0	117	14	US-10-223-087-6
29	609	100.0	117	14	US-10-223-087-6
30	609	100.0	117	14	US-10-011-692A-6
31	609	100.0	117	14	US-10-006-768A-6
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33	609	100.0	117	14	US-10-006-063A-6
34	609	100.0	117	14	US-10-020-063A-6
35	609	100.0	117	14	US-10-223-083-6
36	609	100.0	117	14	US-10-015-391A-6
37	609	100.0	117	14	US-10-223-089-6
38	609	100.0	117	14	US-10-017-407A-6
39	609	100.0	117	14	US-10-011-833A-6
40	609	100.0	117	14	US-10-006-041A-6
41	609	100.0	117	14	US-10-015-822A-6
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44	609	100.0	117	14	US-10-006-172A-6
45	609	100.0	117	14	US-10-017-253A-6

ALIGNMENTS

RESULT 1
US-09-946-374-6
Sequence 6, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 609; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVGMAVFLASRLGGGLLTLEBHAHFLGTGAATTWNSCICRDSGTDSDVDTQ 60
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RESULT 2

US-10-061-056-6
Sequence 6, Application US/10081056
Publication No. US20040043927A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Masters, Scott A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey

APPLICANT: Ye, Weilian

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235P1C1

CURRENT APPLICATION NUMBER: US/10/061,056

PRIOR APPLICATION NUMBER: PCT/US01/21735

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 60/219,556

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/220,624

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,664

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/222,695

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: US 09/643,657

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: PCT/US00/23522

PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
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PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
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PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-03-14
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PRIOR FILING DATE: 2001-03-22
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PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/18692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 363

SEQ ID NO 6
LENGTH: 117
TYPE: PRT

ORGANISM: Homo sapiens

US-10-061-056-6

Query Match 100.0%; Score 609; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MIVGWAVFLASRLGGCLLTLEHIAFLGTGATWNSCICRDBSDGTDSDVTOQ 60
 Oy 61 QQAENSAVFTADTSSQPRDPVPRRGGRGPRPRKKONVDGLVLDPLAVIRTLVTK 117
 Db 61 QQAENSAVFTADTSSQPRDPVPRRGGRGPRPRKKONVDGLVLDPLAVIRTLVTK 117

RESULT 3

US-10-066-500-9
 Sequence 9, Application US/10066500
 Publication No. US20020177165A1
 GENERAL INFORMATION:
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Botstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
 APPLICANT: Hanspeter Gerber
 APPLICANT: Mary E. Gerritsen
 APPLICANT: Audrey Goddard
 APPLICANT: Paul J. Godowski
 APPLICANT: Austin L. Gurney
 APPLICANT: Ivar J. Kjaavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zeng
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3130R1C7
 CURRENT FILING DATE: 2002-02-01
 PRIOR APPLICATION NUMBER: 10/002,796
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059115
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PRIOR APPLICATION NUMBER: 60/079294
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 PRIOR APPLICATION NUMBER: 09/333077
 PRIOR FILING DATE: 1999-06-14
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PRIOR FILING DATE: 1999-08-25
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 PRIOR FILING DATE: 1999-08-25
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 PRIOR APPLICATION NUMBER: 09/423741
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: 09/423844
 PRIOR FILING DATE: 1999-11-12
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 PRIOR APPLICATION NUMBER: PCT/US99/20111
 PRIOR FILING DATE: 1999-09-01
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 13; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MIVGMAVFASRSIGGILLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQ 60
 Db 1 MIVGMAVFASRSIGGILLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQ 60

Cy 61 QQAENSAPFADTRSPDRDVPFRPRRGHPEBRKKONVDGLVLTAVIRTLVDK 117
 Db 61 QQAENSAPFADTRSPDRDVPFRPRRGHPEBRKKONVDGLVLTAVIRTLVDK 117

RESULT 4
 US-10-002-796-9
 Sequence 9, Application US/10002796
 Publication No. US20030032057A1
 GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Botstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
 APPLICANT: Hanspeter Gerber
 APPLICANT: Mary E. Gerltsen
 APPLICANT: Audrey Goddard
 APPLICANT: Paul J. Godowski
 APPLICANT: Austin L. Gurney
 APPLICANT: Ivar J. Kjaevan
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zang
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3130R1C1
 CURRENT APPLICATION NUMBER: US/10/002,796
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 100.0%; Score 609; DB 14; Length 117;
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Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MIVFGMAVFLASRSIGGLITTEHTAHLGTGAATNGNSCICBDSGTDSDVDTQQ 60
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DB 61 QOENSANPTDTSQRPDRPRRGSGPBRKKNVDGLVDTLAVIRTLVDK 117

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RESULT 5
US-10-066-273-9
Sequence 9, Application US/10066273
Publication No. US20030032062A1
GENERAL INFORMATION:
APPLICANT: Avi U. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Garney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tuma
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zhang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P130R1C2
CURRENT APPLICATION NUMBER: US/10/066,273
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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Query Match 100.0%; Score 609; DB 14; Length 117;
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RESULT 6

US-10-066-494-9
Sequence 9, Application US/10066494
Publication No. US20030032063A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
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APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
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 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 09/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGAVFLASRISGGILLTLEHIAHFLGTGGAATTGNSCTCRDSDGTDBSDVDVQ 60
 Db 1 MIVFGAVFLASRISGGILLTLEHIAHFLGTGGAATTGNSCTCRDSDGTDBSDVDVQ 60
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 Db 61 QQAENSAYFTADTRQOPDPVPRRGRGPHPRRKKONVDGLVDTLAVIRTLVX 117

RESULT 7
 US-10-066-269-9
 Sequence 9, Application US/10066269
 Publication No. US20030040014A1

GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Borstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gertlisen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Klavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
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APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P9130R1C4
CURRENT FILING DATE: 2002-02-01
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PRIOR FILING DATE: 2001-11-15
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Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 6, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
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; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: Signal peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 22-25, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
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US-10-066-856A-6

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Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 QOSENSAVPTADTRSGPRDPVRRPGRGPHPRKKQNDGLVDTLAVIRTLVDK 117

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RESULT 9
US-10-066-211-9
; Sequence 9, Application US/10066211
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kjaevlin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni

```

APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P Mickey Williams
 APPLICANT: William T. Wood
 APPLICANT: Zemin Zang
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3130R1C8
 CURRENT FILING DATE: 2002-02-01
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 PRIOR APPLICATION NUMBER: PCT/US99/22547

Query Match 100.0%; Score 609; DB 14; Length 117;
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RESULT 10
 US-10-066-193-9
 Sequence 9, Application US/10066193
 Publication No. US20030044902A1
 GENERAL INFORMATION:
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Botstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleon Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
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 APPLICANT: Mary E. Gertlisen
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 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas

APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zang
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P130R1C3
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/423844
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/709228
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/808689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/870574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 09/872035

PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: PCT/US98/25190
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1998-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1,7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYFGWAVFLASLSLQGLLTLEHIAFLTGGAATMGSCICRDSGTDSDVDTQ 60
DB 1 MYFGWAVFLASLSLQGLLTLEHIAFLTGGAATMGSCICRDSGTDSDVDTQ 60

QY 61 QQAENSAVPTADTRSPDRDPVPRPRGRGPHBPRRKKQVNDGIVDTLAVIRTLVXK 117
DB 61 QQAENSAVPTADTRSPDRDPVPRPRGRGPHBPRRKKQVNDGIVDTLAVIRTLVXK 117

RESULT 11
US-10-006-818A-6
Sequence 6, Application US/10006818A
Publication No. US20030054406A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deeneyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C
CURRENT APPLICATION NUMBER: US/10/006,818A
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 6
LENGTH: 117
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-16
OTHER INFORMATION: Signal Peptide
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
OTHER INFORMATION: N-Myristoylation Site.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 22-26, 50-54, 113-117
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-818A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
DB 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
QY 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117
DB 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117

RESULT 12

US-10-015-393A-6
Sequence 6, Application US/10015393A
Publication No. US20030069179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC46
CURRENT APPLICATION NUMBER: US/10/015,393A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 6
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-16
OTHER INFORMATION: Signal Peptide
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
OTHER INFORMATION: N-Myristoylation Site.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 22-26, 50-54, 113-117
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-393A-6

Query Match 100.0%; Score 609; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
DB 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
QY 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117
DB 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117

RESULT 13

US-10-015-869A-6
Sequence 6, Application US/10015869A
Publication No. US20030073130A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC45
CURRENT APPLICATION NUMBER: US/10/015,869A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 6
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-16
OTHER INFORMATION: Signal Peptide
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
OTHER INFORMATION: N-Myristoylation Site.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 22-26, 50-54, 113-117
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-869A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
DB 1 MIVFGMAVFLASRLGGGLLTLEEHIAHFLGTGAATTMNSCICRDSGTDSDVDTQQ 60
QY 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117
DB 61 QOENSAYVTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117

RESULT 14

US-10-012-121A-6
Sequence 6, Application US/10012121A
Publication No. US20030073810A1

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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC20
CURRENT APPLICATION NUMBER: US/10/012,121A
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 6
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-16
OTHER INFORMATION: Signal Peptide
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
OTHER INFORMATION: N-Wyrietoystation Site.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 22-26, 50-54, 113-117
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-012-121A-6

Query Match          100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGGAATTMGNSCICRDSGTDSDYDTQC 60
DB 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGGAATTMGNSCICRDSGTDSDYDTQC 60
QY 61 QQAENSAPVPTADTRSPQPRDPVPRRGRGPHERRRKKQNVDGVLDTLAVITLVXK 117
DB 61 QQAENSAPVPTADTRSPQPRDPVPRRGRGPHERRRKKQNVDGVLDTLAVITLVXK 117

RESULT 15
US-10-006-116A-6
Sequence 6, Application US/10006116A
Publication No. US20030082626A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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FILE REFERENCE: P2830PIC15
CURRENT APPLICATION NUMBER: US/10/006,116A
CURRENT FILING DATE: 2001-12-16
Prior Application Number: 60/098716
Prior Filing Date: 1998-09-01
Prior Application Number: 60/098723
Prior Filing Date: 1998-09-01
Prior Application Number: 60/098749
Prior Filing Date: 1998-09-01
Prior Application Number: 60/098750
Prior Filing Date: 1998-09-01
Prior Application Number: 60/098803
Prior Filing Date: 1998-09-02
Prior Application Number: 60/098821
Prior Filing Date: 1998-09-02
Prior Application Number: 60/098843
Prior Filing Date: 1998-09-02
Prior Application Number: 60/099536
Prior Filing Date: 1998-09-09
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Prior Filing Date: 1998-09-09
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Prior Filing Date: 1998-09-16
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Prior Filing Date: 1998-09-16
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Prior Application Number: 60/100711
Prior Filing Date: 1998-09-17
Prior Application Number: 60/100848
Prior Filing Date: 1998-09-18
Prior Application Number: 60/100849
Prior Filing Date: 1998-09-18
Prior Application Number: 60/100919
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Mon Apr 5 09:54:04 2004

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Page 17

PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-29
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PRIOR APPLICATION NUMBER: 60/102687
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PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
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PRIOR FILING DATE: 1998-10-07
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PRIOR FILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
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PRIOR APPLICATION NUMBER: 60/105169
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PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105882
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106023
PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGAVFLASRSIGGILLTLEHIAFLGTGAATTMGSCICRDDSGETDSVDVQ 60
DB 1 MIVFGAVFLASRSIGGILLTLEHIAFLGTGAATTMGSCICRDDSGETDSVDVQ 60
QY 61 QQENSAVPTADTRSGPRDPVAPRRGRGPHPRRKKQVNDGLVDTLAVIRTVDX 117
DB 61 QQENSAVPTADTRSGPRDPVAPRRGRGPHPRRKKQVNDGLVDTLAVIRTVDX 117

Search completed: April 2, 2004, 09:56:13
Job time: 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:37:06 ; Search time 39 seconds
(without alignments)

946.555 Million cell updates/sec

Title: US-10-066-500-9

Perfect score: 609
Sequence: 1 MIVFGWAVFLASRLSGGL.....QNVDSGLVDTLAVIRLVK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rotent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	99.2	576	4 Q96DX4	Q96DX4 homo sapien
2	586	96.2	576	6 Q95LP3	Q95LP3 macaca fasc
3	561	92.1	117	11 Q8BLS8	Q8BLS8 mus musculu
4	556	91.3	576	11 Q8C039	Q8C039 mus musculu
5	556	91.3	576	11 Q8BVR6	Q8BVR6 mus musculu
6	86	14.1	601	16 Q82F17	Q82F17 streptomyce
7	85.5	14.0	290	5 Q20394	Q20394 caenorhabdi
8	79.5	13.1	356	10 Q9ATP4	Q9ATP4 oryza sativ
9	79.5	13.1	388	10 Q941M8	Q941M8 oryza sativ
10	79.5	13.1	388	10 Q8LNE8	Q8LNE8 oryza sativ
11	79.5	13.1	388	10 Q7Y1X7	Q7Y1X7 oryza sativ
12	79.5	13.1	388	10 Q9VXR3	Q9VXR3 drosophila
13	79	13.0	970	10 Q9ATP2	Q9ATP2 oryza sativ
14	79	13.0	970	10 Q7XP23	Q7XP23 oryza sativ
15	78.5	12.9	188	2 Q7WX07	Q7WX07 alcaligenes
16	78	12.8	179	5 Q9XZ40	Q9XZ40 plasmodium

17	78	12.8	191	5 Q9UC01	Q9UC01 plasmodium
18	78	12.8	203	5 Q9UC00	Q9UC00 plasmodium
19	78	12.8	480	5 Q27033	Q27033 theileria p
20	77.5	12.7	550	12 Q40912	Q40912 kaposi's sa
21	77.5	12.7	550	12 P88903	P88903 kaposi's sa
22	76.5	12.6	634	4 Q8IXW0	Q8IXW0 homo sapien
23	76	12.5	1063	16 Q8XXH5	Q8XXH5 ralestonia s
24	75.5	12.4	948	5 Q9U104	Q9U104 caenorhabdi
25	75	12.3	147	5 Q15805	Q15805 plasmodium
26	75	12.3	183	5 Q9U0B5	Q9U0B5 plasmodium
27	75	12.3	183	5 Q9U0B6	Q9U0B6 plasmodium
28	75	12.3	204	5 Q9U0B4	Q9U0B4 plasmodium
29	75	12.3	260	5 Q81T83	Q81T83 plasmodium
30	75	12.3	267	13 Q9PUV0	Q9PUV0 baistes sp
31	75	12.3	278	5 Q25862	Q25862 plasmodium
32	75	12.3	291	5 Q25789	Q25789 plasmodium
33	74.5	12.2	121	12 Q8QRK4	Q8QRK4 hepatitis c
34	74.5	12.2	462	3 Q42721	Q42721 penicillium
35	74.5	12.2	2120	5 Q81AK1	Q81AK1 plasmodium
36	74	12.2	850	16 Q8FML9	Q8FML9 corynebacte
37	73.5	12.1	416	12 Q81265	Q81265 hepatitis c
38	73	12.0	206	5 Q9U0C3	Q9U0C3 plasmodium
39	73	12.0	220	5 Q9U0B3	Q9U0B3 plasmodium
40	73	12.0	222	5 Q9U0B1	Q9U0B1 plasmodium
41	73	12.0	353	11 Q62313	Q62313 mus musculu
42	73	12.0	579	2 Q8GFP2	Q8GFP2 streptomyce
43	73	12.0	1160	4 Q8T0V9	Q8T0V9 drosophila
44	73	12.0	1163	4 Q8N6U4	Q8N6U4 homo sapien
45	73	12.0	3571	10 Q9S127	Q9S127 arabidopsis

ALIGNMENTS

RESULT 1

Q96DX4 PRELIMINARY; PRT; 576 AA.

AC Q96DX4; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein KIAA1972.
GN KIAA1972.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lymph;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21642142; PubMed=11853119;
RA Nagase T.; Kikuno R.; Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XXII.
RT The complete sequences of 50 new cDNA clones which code for large

RT proteins.";
RL DNA Res. 8:319-327(2001).
DR EMBL: BC013173; AAH13173.1; -;
DR EMBL: AB075852; BAB85558.1; -;
DR InterPro: IPR008938; ARM
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00622; SPRY_1.
DR SMART: SM00184; RING_1.
DR SMART: SM00449; SPRY_1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Hypothetical protein
SQ SEQUENCE 576 AA; 64180 MW; 8598E43E96691F9B CRC64;

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Query Match          99.2%; Score 604; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60
DB 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 2
Q95LUP3 PRELIMINARY; PRT; 576 AA.
AC Q95LUP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein.
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB072745; BAB69714.1; -.
DR InterPro: IPR008938; APW.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Hypothetical protein.
SQ SEQUENCE 576 AA; 64255 MW; 68D230AD1C4F58D CRC64;

Query Match          96.2%; Score 586; DB 6; Length 576;
Best Local Similarity 97.4%; Pred. No. 1.1e-55;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60
DB 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 3
Q98LUS8 PRELIMINARY; PRT; 117 AA.
AC Q98LUS8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical Sp1a and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;

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RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL: AK043522; BAC31566.1; -.
KM Hypothetical protein.
SQ SEQUENCE 117 AA; 12738 MW; D3FEC471ABD5D3C CRC64;

Query Match          92.1%; Score 561; DB 11; Length 117;
Best Local Similarity 91.5%; Pred. No. 9.5e-54;
Matches 107; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60
DB 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 117
DB 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 117

RESULT 4
Q8C039 PRELIMINARY; PRT; 576 AA.
AC Q8C039;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical Sp1a and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL: AK032416; BAC27858.1; -.
DR WGD; MG1:1914860; 4930470D19R1X.
DR InterPro: IPR008938; APW.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Hypothetical protein.
SQ SEQUENCE 576 AA; 64340 MW; D72D60E80311D02 CRC64;

Query Match          91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60
DB 1 MIVFGMAVFLASRLGQGLLTLEEHIAFLGTGAATTMGNSCICRDSGTDSDVDTQ 60

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 5
Q8BVR6 PRELIMINARY; PRT; 576 AA.

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AC Q8BYR6; 08BYR6; (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical SPL and the Ryanodine receptor (Hypothetical protein)
 GN 4930470D19R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
 RA Datchenko L., Marzina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Pirange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosnak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Tissue=Embryo;
 RX Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK076799; BAC36485.1;
 DR EMBL: BC054121; AAHS4121.1;
 DR MGD: MGI:191460; 4930470D19R1K.
 DR InterPro: IPR008938; AKM.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR018411; Znf_ring.
 DR Pfam: PF00622; SPRY.1.
 DR SMART: SM00184; RING.1.
 DR SMART: SM00449; SPRY.1.
 DR PROSITE: PS00689; ZF_RING_2; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 576 AA; 64322 MW; 823C9532FCB13987 CRC64;
 QY Query Match 91.3%; Score 556; DB 11; Length 576;
 DB Best Local Similarity 91.4%; Pred. No. 2.2e-52;
 Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MIVEGMAVFLASRSIGGILLTLEHTAHFLGSGAATNGSCICRDSGTSVDTQ 60
 DB 1 MIVFMAVFLASRSIGGILLTLEHTAHFLGSGAATNGSCICRDSGTSVDTQ 60
 QY 61 QQAENSAPVLTADTRSGPRDPVPRPRGRGPRPRRKKQNDGLVLTAVIRTLVD 116
 DB 61 QQAENSAPVLTADTRSGPRDPVPRPRGRGPRPRRKKQNDGLVLTAVIRTLVD 116

RESULT 6
 Q82F17 PRELIMINARY; PRT; 601 AA.
 AC Q82F17;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Putative thiamine biosynthesis protein.
 GN THIA OR SAV4265.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shida T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shida T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis."
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP005038; BAC11977.1;
 DR GO: GO:0009228; P:Chitin biosynthesis; ISA.
 DR InterPro: IPR002817; Thic.
 DR Pfam: PF01964; Thic.1.
 DR Prodom: PD007048; Thic.1.
 DR TIGRFAMs: TIGR00190; Thic.1.
 KM Complete proteome.
 SQ SEQUENCE 601 AA; 66485 MW; B149CD75A602FCF5 CRC64;
 QY Query Match 14.1%; Score 86; DB 16; Length 601;
 DB Best Local Similarity 32.3%; Pred. No. 0.86;
 Matches 31; Conservative 7; Mismatches 36; Indels 22; Gaps 4;
 QY 39 TMGNSCICRDSG--TDSVDTQOOQA-----NSAVPTADTRSGPRDPVPR----- 83
 DB 55 TMGNSVLYLTSGGYDPSVDTVVRGLAPLRNMWLTARGDIEFYAGRVREDDSGIKRT 114
 QY 84 -PRRGRC-----PHEPRRKKQNDGLVLTAVIR 112
 DB 115 SPRGLRLDAVFPGRPRGRGRDQAVYQLAYAR 150
 QY RESULT 7
 Q03034 PRELIMINARY; PRT; 290 AA.
 AC Q03034;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE F44D12.6 protein.
 GN F44D12.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Rhabditidae;
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coles L.;


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RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z68298; CAA92602.1; -.
DR PIR; T22161; T22161.
DR WormPep; F44D12.6; CE03330.
SQ SEQUENCE 290 AA; 32831 MW; B60BEPE9C89E7780 CRC64;

Query Match
Best Local Similarity 14.0%; Score 85.5; DB 5; Length 290;
Matches 27; Conservative 15; Mismatches 31; Indels 17; Gaps 5;

QY 24 EEHIAHFGTGAATTGNN-SCICRDSGTD-----DSVDTQQAQNSAVPTADTRSQP 77
DB 154 DAHV-HMETGIAFIIRNDACRSKDDGCDTIDSONSKEDQERSKYNSEWPLSD----- 207
QY 78 RDPVPPRRGQPHPRKXQNVGJVDLT 107
DB 208 KKPDRKPPQ-----ETPRRSKORTPGPMPT 232

RESULT 8
Q9ATR4 PRELIMINARY; PRT; 356 AA.
ID Q9ATR4;
AC Q9ATR4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Teosinte branched protein (Fragment).
GN TBL.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21165336; PubMed=11264415;
RA Lukens L., Doebley J.,
RT "Molecular evolution of the teosinte branched gene among maize and
  related grasses."
RL Mol. Biol. Evol. 18:627-638(2001).
DR EMBL; AF322143; AAK37505.1; -.
DR Gramene; Q9ATR4; -.
DR InterPro; IPR005333; TCP.
DR Pfam; PF03634; TCP; 1.
FT NON_TER 356 356
FT NON_TER 1 1
SQ SEQUENCE 356 AA; 37757 MW; 95D7174BC6AB8F84 CRC64;

Query Match
Best Local Similarity 13.1%; Score 79.5; DB 10; Length 356;
Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVTQQAQNSA-----VPTADTRSQPDPVPPRRGQPHPR 93
DB 180 SSVCEDDGSSLSVDKQOQHSPADRGAGADHKGAAHGSHDGGKPAKPRRAANPKRP 239
QY 94 RR 95
DB 240 RR 241

RESULT 9
Q941N6 PRELIMINARY; PRT; 388 AA.
ID Q941N6;
AC Q941N6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Teosinte branched protein.
GN TBL.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. indica guangju'at 4;
RA Hu W., Zhao Y., Luo D.,
RT "The structural and functional analysis of a Tbl-like gene in rice."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043215; AAL05595.1; -.
DR Gramene; Q941N6; -.
DR InterPro; IPR005333; TCP.
DR Pfam; PF03634; TCP; 1.
SQ SEQUENCE 388 AA; 41493 MW; 700B90C018BC66A0 CRC64;

Query Match
Best Local Similarity 13.1%; Score 79.5; DB 10; Length 388;
Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVTQQAQNSA-----VPTADTRSQPDPVPPRRGQPHPR 93
DB 179 SSVCEDDGSSLSVDKQOQHSPADRGAGADHKGAAHGSHDGGKPAKPRRAANPKRP 238
QY 94 RR 95
DB 239 RR 240

RESULT 10
Q8LN68 PRELIMINARY; PRT; 388 AA.
ID Q8LN68;
AC Q8LN68;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Teosinte branched protein.
GN OSUNBA0004G17.5 OR OSTB1.
OS Oryza sativa (Japanese cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCB1_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan O., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Taitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utechtack T.T., Feldlyum T.V.,
RA Yang Q.Q., Haas B.J., Sun B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBA0004G17 genomic sequence."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RA Takeda T., Suwa Y., Ueguchi-Tanaka M., Ashikari M., Matsuo M.,
RA Ueguchi C.;
RT "The OSTB1 gene negatively regulates lateral branching in rice."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC091775; AAM97162.1; -.
DR EMBL; AB088343; AAC54954.1; -.
DR Gramene; Q8LN68; -.
DR InterPro; IPR005333; TCP.
DR Pfam; PF03634; TCP; 1.
SQ SEQUENCE 388 AA; 41504 MW; 8CF363D2EAA02743 CRC64;

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Query Match 13.1%; Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7; Indels 9; Gaps 1;
 Matches 20; Conservative 6; Mismatches 27

QY 43 SCICRDSGTDSVDTQQAENSA-----VPTADTRSGPRDPVPPRRGRGPHPP 93
 179 SSVCEEDSSSLSYDGKQOQHNPADRGAGADHKGAHGHSDGKPKAPRRRAANPKPP 238

QY 94 RR 95
 239 RR 240

Db

RESULT 11
 ID QY1X7 PRELIMINARY; PRT; 388 AA.
 AC QY1X7
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tescinte-branching 1.
 GN TBI.
 OS Oryza sativa (indica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39946;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. IR-36;
 RA Hu W., Zhang S., Zhao Z., Zhao Y., Sun C.R., Luo D.;
 RT "The structural and expression analysis of OST1 in rice."
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY266002; AAP371176.1;
 SQ SEQUENCE 388 AA; 41504 MW; 8CF363DEBA02743 CRC64;

Query Match 13.1%; Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7; Indels 9; Gaps 1;
 Matches 20; Conservative 6; Mismatches 27

QY 43 SCICRDSGTDSVDTQQAENSA-----VPTADTRSGPRDPVPPRRGRGPHPP 93
 179 SSVCEEDSSSLSYDGKQOQHNPADRGAGADHKGAHGHSDGKPKAPRRRAANPKPP 238

QY 94 RR 95
 239 RR 240

Db

RESULT 12
 ID QYXR3 PRELIMINARY; PRT; 5146 AA.
 AC QYXR3
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE CG8184 protein.
 GN CG8184.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkelley;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Peiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 BA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 BA Beeson K.Y., Benos P.V., Bereman B.P., Bhattacharya D., Bolshakov S.,
 BA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 BA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 BA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 BA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 BA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 BA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
 BA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 BA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 BA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 BA Hostin D., Houston K.A., Howland T.U., Wei M.-H., Ibegwan C.,
 BA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 BA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 BA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 BA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 BA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 BA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 BA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 BA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 BA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 BA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 BA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 BA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 BA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 BA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 BA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 BA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 BA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amaratilake P.G., Brandon R.C., Rogers Y.,
 RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresner D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Paclet J., Paragae V., Park S., Patel S., Peiffer B.,
 RA Prounenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Mathews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bereman B., Carlson J.W., Ceiniker S.E.,
 RA Clamp W., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn B., Richter J., Russo S.,
 RA Searle S.M.J., Smith B., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AEO03500; AAF49495.2;
 DR FlyBase; FBgn0030674; CG8184.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.

DR GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO:0006810; P:transport; IEA.
 DR GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro: IPR008938; ARM.
 DR InterPro: IPR000569; HECT domain.
 DR InterPro: IPR001993; Mitoch carrier.
 DR InterPro: IPR000449; UBA domain.
 DR InterPro: IPR004170; WME_dom.
 DR Pfam: PF0632; HECT; 1.
 DR Pfam: PF02825; UBA; 1.
 DR Pfam: PF02825; WME; 1.
 DR SMART: SM00119; HECTC; 1.
 DR PROSITE: PS00237; HECT; 1.
 DR PROSITE: PS00315; MITOCH_CARRIER; 1.
 DR PROSITE: PS00310; UBA; 1.
 SQ SEQUENCE 5146 AA; 556847 MW; 27BF187F2D279846 CRC64;

Query Match 13.1%; Score 79.5; DB 5; Length 5146;
 Best Local Similarity 30.1%; Pred. No. 54;
 Matches 22; Conservative 8; Mismatches 30; Indels 13; Gaps 2;

QY 32 GTGGAATTGNSCTCRDSDGTDSDVDTQCGQAENSVAFTADTRSQPRDPVPPRRKKGPH 91
 DB 853 GTGSASVYLGAGADTNDSSGDDDDDDDEMSA-----SQCGQQTTPGQGGGFS 901

QY 92 EPRRKQNVGLV 104
 DB 902 TPR--TQAGGVV 912

RESULT 13

QYAF2 PRELIMINARY; PRT; 970 AA.
 AC Q9AF2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to Zea mays chromosome 42kDazein-associated intercluster
 DE region, copia-type polyploid protein.
 GN OSJNB0094J09.18.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
 RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
 RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toch K.,
 RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
 RT "Genomic Sequence for Oryza sativa, Nipponbare strain, Chromosome X,
 RT Clome OSJNB0094J09, complete sequence."
 RN Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R.;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bai H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
 RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
 RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toch K.,
 RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC078839; AAK13102.1; -
 DR Gramene: Q9AF2; -
 DR GO:0003677; F:DNA binding; IEA.
 DR GO:0004269; F:subtilase activity; IEA.

DR GO:0006310; P:DNA recombination; IEA.
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR00209; Peptidase_58.
 DR InterPro: IPR001584; Rve.
 DR Pfam: PF00665; Rve; 1.
 DR PROSITE: PS00136; SUBTILASE ASP; 1.
 SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match 13.0%; Score 79; DB 10; Length 970;
 Best Local Similarity 27.4%; Pred. No. 8; 8;
 Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGNAVFLASRLG---QGLLTLEHIAHFLGT-----GGAATM--GNSCTCRDD 49
 DB 551 YSNVFMATKDEAFQFRGLFLRD---LEFGSLKIRSDNGTISQVGBSDSCIFEDD 607

QY 50 SGTDDSVDTQCGQAENSVAFTADTRSQPRDPVPPRRKKGPHPRKKQNVG 102
 DB 608 SDDDDKVGSGAGGTGRAGGTAST-----FP--GRPPDERNRGSSG 649

RESULT 14

QYAF23 PRELIMINARY; PRT; 970 AA.
 AC Q7XF23;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to Zea mays chromosome 42kDazein-associated intercluster
 DE region, copia-type polyploid protein.
 GN OSJNB0094J09.18.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RC Buell C.R., Ming R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE017089; AAP53536.1; -
 KW Polypeptide.
 SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;
 Query Match 13.0%; Score 79; DB 10; Length 970;
 Best Local Similarity 27.4%; Pred. No. 8; 8;
 Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGNAVFLASRLG---QGLLTLEHIAHFLGT-----GGAATM--GNSCTCRDD 49
 DB 551 YSNVFMATKDEAFQFRGLFLRD---LEFGSLKIRSDNGTISQVGBSDSCIFEDD 607

QY 50 SGTDDSVDTQCGQAENSVAFTADTRSQPRDPVPPRRKKGPHPRKKQNVG 102
 DB 608 SDDDDKVGSGAGGTGRAGGTAST-----FP--GRPPDERNRGSSG 649

RESULT 15

QYAF23 PRELIMINARY; PRT; 188 AA.
 AC Q7WX07;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative single-strand binding protein.

GN SSB OR PHG335.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OG Plasmid megaplasmid phg1.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_Taxid=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16;
 RA Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
 RT "Complete Nucleotide Sequence of phg1: A Ralstonia eutropha H16
 RT Megaplasmid Encoding Key Enzymes of H2-based Lithoautotrophy and
 RT Anaerobiosis.";
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY05378; MAP86084.1; -.
 KW Plasmid.
 SQ SEQUENCE 188 AA; 20451 MW; B43832FBC232CF4 CRC64;

Query Match 12.9%; Score 78.5; DB 2; Length 188;
 Best Local Similarity 33.8%; Pred. No. 1.5;
 Matches 26; Conservative 8; Mismatches 30; Indels 13; Gaps 5;

QY 32 GTGGAATTGNSCTCRDSDGTDSDVDTQQQAENS AVPTADTRSQP--RDPVRRPPRRRG 89
 Db 110 GGGGASD--GDS-----DSGTRASASQSPASASAPGQ--RQPPARQAPAPSPNGFG 161

QY 90 PHE--PRRKQNVGG 103

Db 162 DFNEDIPFAPAPADGI 178

Search completed: April 2, 2004, 09:54:13
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:51:52 ; Search time 22 Seconds
(without alignments)
274.556 Million cell updates/sec

Title: US-10-066-500-9

Perfect score: 1 MIFGMAVFLASRLGGGL.....QNVGLVLDLAVIRLVK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUTS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	13.1	460	US-09-252-991A-20180	Sequence 20180, A
2	79	13.0	287	US-09-252-991A-30267	Sequence 30267, A
3	78	12.8	1527	US-09-418-710-27	Sequence 27, Appl
4	78	12.8	1531	US-09-418-710-39	Sequence 29, Appl
5	75	12.3	433	US-08-466-120-2	Sequence 2, Appl
6	75	12.3	433	PCT-US94-07266-2	Sequence 2, Appl
7	75	12.3	1525	US-09-418-710-69	Sequence 69, Appl
8	74.5	12.2	462	US-08-865-597A-2	Sequence 2, Appl
9	73.5	12.1	2509	US-08-149-097D-35	Sequence 35, Appl
10	73	12.0	623	US-09-029-348-3	Sequence 3, Appl
11	73	12.0	626	US-09-029-348-2	Sequence 2, Appl
12	72.5	11.9	333	US-09-252-991A-28443	Sequence 28443, A
13	71.5	11.7	562	US-09-252-991A-20178	Sequence 20178, A
14	71.5	11.7	566	US-09-252-991A-18531	Sequence 18531, A
15	71	11.7	863	US-09-252-991A-26059	Sequence 26059, A
16	70	11.5	396	US-09-252-991A-32927	Sequence 32927, A
17	69	11.3	191	US-08-290-665A-198	Sequence 198, App
18	69	11.3	191	US-08-290-665A-199	Sequence 199, App
19	69	11.3	191	US-08-290-665A-200	Sequence 200, App
20	69	11.3	191	US-08-290-665A-201	Sequence 201, App
21	69	11.3	191	US-08-290-665A-202	Sequence 202, App
22	69	11.3	191	US-08-290-665A-203	Sequence 203, App
23	69	11.3	191	PCT-US95-10398-198	Sequence 198, App
24	69	11.3	191	PCT-US95-10398-199	Sequence 199, App
25	69	11.3	191	PCT-US95-10398-200	Sequence 200, App
26	69	11.3	191	PCT-US95-10398-201	Sequence 201, App
27	69	11.3	191	PCT-US95-10398-202	Sequence 202, App

28	69	11.3	191	5	PCT-US95-10398-203	Sequence 203, App
29	69	11.3	319	4	US-08-635-886C-226	Sequence 226, App
30	69	11.3	319	4	US-08-974-690C-226	Sequence 226, App
31	69	11.3	350	4	US-09-252-991A-19537	Sequence 19537, A
32	69	11.3	498	4	US-09-354-151-2	Sequence 2, Appl
33	69	11.3	778	4	US-09-198-452A-508	Sequence 508, App
34	68.5	11.2	788	2	US-08-918-914-4	Sequence 4, Appl
35	68	11.2	149	4	US-09-252-991A-21599	Sequence 21599, A
36	68	11.2	379	4	US-09-252-991A-31693	Sequence 31693, A
37	68	11.2	882	3	US-09-413-814-78	Sequence 78, Appl
38	67.5	11.1	518	4	US-09-252-991A-18753	Sequence 18753, A
39	67.5	11.1	727	4	US-08-475-844-9	Sequence 9, Appl
40	67.5	11.1	727	5	PCT-US95-08429-9	Sequence 9, Appl
41	67.5	11.1	1298	2	US-08-690-473-2	Sequence 2, Appl
42	67.5	11.1	1298	3	US-09-259-821A-2	Sequence 2, Appl
43	67.5	11.1	1298	3	US-08-843-659-2	Sequence 2, Appl
44	67	11.0	393	4	US-09-432-470-2	Sequence 2, Appl
45	67	11.0	393	4	US-09-432-470-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-252-991A-20180
; Sequence 20180, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20180
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20180

Query Match      13.1%; Score 80; DB 4; Length 460;
Best Local Similarity 28.6%; Pred. No. 0.42; 23; Indels 16; Gaps 2;
Matches 20; Conservative 11; Mismatches

QY      32  GTGGAATTGNGCICRDSVDTQQQAENSAPVPAATRSQPRDPFRPRGRGPH 51
      373  GCGQAIVGAG-----EQADPEQRARVPGAIQA-----NNGEDVPEPPGERGRDH 416
      417  EQRCGRHVD 426

Db
QY      92  EPRRKQNTD 101
      417  EQRCGRHVD 426

RESULT 2
US-09-252-991A-30267
; Sequence 30267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30267
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30267

Query Match      13.0%; Score 79; DB 4; Length 287;
Best Local Similarity 37.5%; Pred. No. 0.3;
Matches 21; Conservative 7; Mismatches 24; Indels 4; Gaps 1;

QY 51 GDDSDVDTQOQQAENS AVPTADTRSGPRDPVPR-----RRGRGHEPRRKQNYDG 102
DB 15 GRDPKRTQQRKRDHPAGVVAARPGPARPRRRPGGLGRGAGKRRRRRQVPG 70

RESULT 3
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match      12.8%; Score 78; DB 4; Length 1527;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDDSVDTQOQQAENS AVPTADTRSGPRDPVPR-----PR-----RRGRGHEPRR 95
DB 1255 EDESDSEEEEEEEDYEVAGLRPRKTRKHSVIPPARSGRRPKKHSTR 1314

QY 96 KK-----QNYDGLVLDLT 107
DB 1315 SQPKAPVDDAEYDELVLQT 1334

RESULT 4
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match      12.8%; Score 78; DB 4; Length 1531;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDDSVDTQOQQAENS AVPTADTRSGPRDPVPR-----PR-----RRGRGHEPRR 95
DB 1259 EDESDSEEEEEEEDYEVAGLRPRKTRKHSVIPPARSGRRPKKHSTR 1318

QY 96 KK-----QNYDGLVLDLT 107
DB 1319 SQPKAPVDDAEYDELVLQT 1338

RESULT 5
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5869284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07266
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

Query Match      12.3%; Score 75; DB 2; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3;

QY 35 GAATTGNSCTCRPDSGTDSDVDTQOQQAENS AVPTA--DTRSQ--PRDP--VRPPRRGRGF 90
DB 29 GSGAQGSSCTLRBEAMPHSAGGTAGVGLAAEPTRALLTRAPPSPPTIRPPKXKKG 88

RESULT 6
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266
```

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GENERAL INFORMATION:
APPLICANT: CAO, ET AL.
TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILAN,
ADDRESSER: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07266
FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 345800-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-07266-2

Query Match 12.3%; Score 75; DB 5; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3.

Cy 35 GATTGAGNSCICRDSGTDSDVDTQCOQAEASAVPTA-DTRSQ-PKDP--VPPRRGRGP 90
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 29 GSGAGGGSCICRREARMPHSGAGTAVGLAEAPFTALLTRAPPSPSTETISPPKXKGP 98

RESULT 7
US-09-418-710-69
Sequence 69, Application US/09418710
Patent No. 6596482
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 1525
TYPE: PRT
ORGANISM: Homo sapiens
US-09-418-710-69

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Query Match 12.3%; Score 75; DB 4; Length 1555;
Best Local Similarity 27.9%; Pred. No. 7.9;
Matches 24; Conservative 12; Mismatches 24; Indels 26; Gaps 4;

QY      48 DDGSTDSDV-----TQQQAENSAVPTADTRESQPRDPV-----PP-----RGR 68
          :::::
          1246 ESSASEDESEDESEEEEEEEEDYEVAIGLRLFRKTRIGKSHVIPPAAERSRRPK 1305
          :::::
          Db      69 GHEPRKK-----QNVGIVLDT 107
          1306 KPHSTRSQPRAPPVDAEVDLVLQT 1331

RESULT 8
US-08-865-597A-2
; Sequence 2, Application US/08865597A
; Patent No. 5973131
; GENERAL INFORMATION:
; APPLICANT: Cao, Liang
; APPLICANT: Yen, Kwok Yung
; TITLE OF INVENTION: PENNICILLUM MARNEFFEI ANTIGENIC PROTEIN 1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,597A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Albert Wai-Kit
; REGISTRATION NUMBER: 36,479
; REFERENCE/DOCKET NUMBER: 50288-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-597A-2

Query Match 12.2%; Score 74.5; DB 2; Length 462;
Best Local Similarity 29.2%; Pred. No. 1.9;
Matches 21; Conservative 10; Mismatches 36; Indels 5; Gaps 1

QY      12 SRSLGGLLTTEHIAHFLGTGCAATTMGSCICRPDSCGSDSVPTQQQAENSAVPTA 71
          :::::
          Db      328 SROLSIGIAGIKKIGDIFAGTGPARTIST-----PEASTAPAPSTPPQTEIDTLVPAT 382
          :::::
          QY      72 DTSQPRDPVPR 83
          383 STAPGAPAPAP 394

RESULT 9
US-08-149-097D-35
; Sequence 35, Application US/08149097D
; Patent No. 5874235
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael

```

```

APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
TITLE OF INVENTION: 40
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,097D
FILING DATE: 05-NOV-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-55038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2509 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
FEATURE:

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OTHER INFORMATION: /product= "Alphala-1 subunit of
OTHER INFORMATION: human calcium channel"
US-08-149-097D-35

Query Match 12.1%; Score 73.5; DB 2; Length 2509;
Best Local Similarity 24.2%; Pred. No. 23;
Matches 31; Conservative 9; Mismatches 39; Indels 49; Gaps 4;

QY 12 SRSLGGSLLTLEHIAHLGTG-----ATTMGNSC----- 44
Db 2251 SRSSSSB-----REHAHRRQSSSVSSPAPSTISGISTPRGRRLQPTSTPRHVSYS 2305
QY 45 -ICRDSGTDDSVDTQCGQAENSAY-----PNAIDTSQRDPVRRPRRG 87
Db 2306 PVIRKAGSGPQQQQQQQQQQAVALPAPGRAATSGPRRYPPTAEPPLAGDRPTGSHSG 2365
QY 88 RGPHEPR 95
Db 2366 RSPMER 2373

RESULT 10
US-09-029-348-3
Sequence 3, Application US/09029348
Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: 0087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 623
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
US-09-029-348-3

Query Match 12.0%; Score 73; DB 3; Length 623;
Best Local Similarity 28.8%; Pred. No. 4.2;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;

QY 16 GGLLTLEH---IAHLGTGGAATMGNS-----CICRDSGT---DSS 55
Db 8 GSWLLALHLPTTILAQGAEEVGGCSHLGSGYADRDVWKPEPCQLTVC--DSGSLCDDI 65
QY 56 V-DTQCGQAENSAYP---TADTSQRDPVRRPRRGGRGHEPR 94
Db 66 ICDDDELDCPNRPIRFEGCAVCPCPPAPTRPP-NGGPGGPK 108

RESULT 11
US-09-029-348-2
Sequence 2, Application US/09029348
Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: 0087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE

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Mon Apr 5 09:54:04 2004

us-10-066-500-9.trai

Page 5

OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-2

Query Match 12.0%; Score 73; DB 3; Length 626;
Best Local Similarity 28.8%; Pred. No. 4.2;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;

QY 16 GGGLLLTLEEH---IAHFLGTGATATWNS-----CICRDSGT---DGS 55
DB 8 GSWLLIALHPIITIAQGEAVGGCSHIGSYADRDVWKPEPCQICVC--DSGSVLCDDI 65
QY 56 V-DTQQQAENSAPV---TADTSQPRDPVPRPRRGSGHEPR 94
DB 66 ICDDDELDPNPEIPFGCCAVCPQPTAPTRPP-NGGPGQCFK 108

RESULT 12

US-09-252-991A-28443
Sequence 28443, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28443
LENGTH: 333
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28443

Query Match 11.9%; Score 72.5; DB 4; Length 333;
Best Local Similarity 27.5%; Pred. No. 2.1;
Matches 25; Conservative 7; Mismatches 24; Indels 35; Gaps 3;

QY 29 HFIQTGAATTWNSCICRDSGTDSVDTQQQAENSAPV---TADTSQPRDPV 82
DB 216 HRLRTGT-----DEGADSGRHHPQAHRRLPLGPDAGDHRRCALPEPR 262
QY 83 P-----PRRGSGHEPRRKX 97
DB 263 QRTGDPAGHREAPGSLRFRPRGHHLFRRR 293

RESULT 13

US-09-252-991A-20178
Sequence 20178, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20178
LENGTH: 562
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20178

Query Match 11.7%; Score 71.5; DB 4; Length 562;
Best Local Similarity 29.7%; Pred. No. 5.5;
Matches 22; Conservative 6; Mismatches 29; Indels 17; Gaps 2;

QY 36 AATTWNSCICRDSGTDSVDTQQQAENSAPVPTADTSQPRDPVPRPRRGSGHEPR-- 93
DB 79 AATPAG-----EDGGQLHGGRPRRLPAGSGAGACPADPRRPGRRRGAQRPP 127
QY 94 ----RKKQNVDCI 103
DB 128 VAGSRARRSGTDAL 141

RESULT 14

US-09-252-991A-18531
Sequence 18531, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18531
LENGTH: 566
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18531

Query Match 11.7%; Score 71.5; DB 4; Length 566;
Best Local Similarity 23.6%; Pred. No. 5.6;
Matches 29; Conservative 10; Mismatches 37; Indels 47; Gaps 4;

QY 23 LEEHIAHFLGTGATATWNSC-ICRDSGTDSVD-----TQQQAENSAPVPTA 71
DB 118 LERLRQPGAGATATRRSSQRIYQADPGRSVDPHGQPPHARRAGSGTEGNAS 177
QY 72 DTRSQPRDP-----VRPR-----GRGHEPRR 95
DB 178 RTRRAPRAPGGQLPAGRGQVROAGDGGARQLRPRRRPAAGTRLLHGPAARRPYPAR 237
QY 96 KQ 98
DB 238 RQR 240

RESULT 15

US-09-252-991A-26099
Sequence 26099, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26099
LENGTH: 863
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099

Query Match 11.7%; Score 71; DB 4; Length 863;
Best Local Similarity 29.1%; Pred. No. 11;
Matches 25; Conservative 8; Mismatches 33; Indels 20; Gaps 3;

Qy	31	LGTCGAATT-----WNSCICRDDSGTSDSDVTQOOQAENSAVPTADT-----RS	75
Db	335	LGPGTAARRTHRPWPGAGGADALRPDAGQADRLRGDPRRSPQADPPAGALRAAGRR	394
Qy	76	QPRDPVVRP-----RGRGPHPRRX	96
Db	395	QPAVPRQPGASGLRRRRGDDHRLRR	420

Search completed: April 2, 2004, 09:55:20
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:35:21 ; Search time 17 Seconds

(without alignments)
358.365 Million cell updates/sec

Title: US-10-066-500-9

Perfect score: 609

Sequence: 1 MIVPGNAVFLASRLSGGL.....QNVGLVDTLAVIRFLVVK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	13.0	612	1	THIC_STRCO
2	78.5	12.9	189	1	SSB_ALCEU
3	78	12.8	1483	1	BALB_HUMAN
4	75	12.3	286	1	MSA2_PLAFL
5	73.5	12.1	2505	1	CCNA_HUMAN
6	73	12.0	281	1	MSA2_PLAFL
7	73	12.0	353	1	TGNI_MOUSE
8	73	12.0	1466	1	CA13_HUMAN
9	72.5	11.9	262	1	MSA2_PLAFL
10	72.5	11.9	272	1	MSA2_PLAFL
11	72.5	11.9	274	1	MSA2_PLAFL
12	72.5	11.9	287	1	MSA2_PLAFL
13	72.5	11.9	300	1	MSA2_PLAFL
14	72.5	11.9	300	1	MSA2_PLAFL
15	72.5	11.9	302	1	MSA2_PLAFL
16	72.5	11.9	347	1	MSA2_PLAFL
17	72.5	11.9	458	1	YB1_CABEL
18	72	11.8	1787	1	CHD3_MOUSE
19	71	11.7	1479	1	BALB_MOUSE
20	70.5	11.6	3726	1	TRX_DROME
21	70	11.5	445	1	NRH_MOUSE
22	69	11.3	1944	1	CHD3_HUMAN
23	68	11.2	424	1	COT1_BOVIN
24	68	11.2	445	1	NRH_MOUSE
25	68	11.2	504	1	FTSY_YEAST
26	68	11.2	702	1	EXO1_YEAST
27	67.5	11.1	399	1	SIR3_HUMAN
28	67.5	11.1	727	1	CTCF_HUMAN
29	67.5	11.1	1298	1	ICP4_HSV1
30	67	11.0	1393	1	C1W4_HUMAN
31	67	11.0	1202	1	NOS3_HUMAN
32	67	11.0	3828	1	TRX_DROVI
33	66.5	10.9	217	1	YK4_EBV

ALIGNMENTS

RESULT 1	ID	THIC_STRCO	STANDARD;	PRT;	612 AA.
34	66.5	10.9	268	1	EP34_HCVNA
35	66.5	10.9	276	1	MSA2_PLAFL
36	66.5	10.9	343	1	GLN2_STVR
37	66.5	10.9	423	1	COT1_HUMAN
38	66.5	10.9	684	1	EP34_HCVNA
39	66	10.8	228	1	EP34_HCVNA
40	66	10.8	228	1	EP34_HCVNA
41	66	10.8	324	1	HE31_STRAW
42	66	10.8	736	1	DVL2_XENLA
43	66	10.8	1021	1	MAPA_MOUSE
44	66	10.8	1380	1	CYNA_LEIDO
45	66	10.8	2716	1	OSA_DROME

THIC_STRCO
ID
THIC_STRCO
STANDARD;
PRT;
612 AA.

AC Q9X9U0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thic.
GN THIC OR SC03928 OR SC011.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=1200953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Baram A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Lathe L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)." / (2002).
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC hydroxymethylpyrimidine) (By similarity).
CC -!- PATHWAY: Thiamine biosynthesis.
CC -!- SIMILARITY: Belongs to the thic family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL/AL39118; CAB4696.1; -
CC PIR/T37181; T37181.
CC HAMAP: MF 00089; -!-
CC InterPro: IPR002817; THIC.
CC Pfam: PF01964; Thic1.
CC ProDom: PD007048; Thic1.
CC TrEMBL: TIGR00190; thic1.
CC Thiamine biosynthesis; Complete proteome
KW
SQ SEQUENCE 612 AA; 67371 MW; 2908F2454200C68 CRC64;
Query Match 13.0%; Score 79; DB 1; Length 612;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 30; Conservative 7; Mismatches 22; Gaps 4;

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QY 39 TWGNSCICRDSG--TDSVDITQOOA-----ENSAVPTADRSQRPDPVAP----- 83
DB 60 TNGQSVTLVDTGPTDPLVDVVRGLAPLENNITARGDEEYAGRPVPEDDGKHT 119
QY 84 -PRRGG-----PHEPRKKONVDGLVDTLAVR 112
DB 120 SPRGGILNDAVFPGRPRQPRGRDGMNAVTLAVAR 155

RESULT 2
SSB_ALCEU STANDARD, PRT, 188 AA.
ID SSB_ALCEU
AC P59927; Q7WX07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Single-strand binding protein (SSB) (Helix-destabilizing protein).
GN SSB OR PHG335.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Plasmid megaplasmid PHG1.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16 / DSM 428 / ATCC 17699;
RA Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
RA Gottschalk G.;
RT "Complete nucleotide sequence of PHG1: a Ralstonia eutropha H16
RT megaplasmid encoding key enzymes of H2-based lithoautotrophy and
RT anaerobiosis."
J. Mol. Biol. 332:369-383 (2003).
CC -1- FUNCTION: This protein is essential for replication of the
CC chromosome. It is also involved in DNA recombination and repair
CC (by similarity).
CC -1- SIMILARITY: Contains 1 SSB domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AY305378; AAP86084.1; -.
CC DR PROSITE; PS00935; SSB; 1.
CC KM DNA-binding; DNA repair; DNA replication; Plasmid.
CC FT DOMAIN 4 109 SSB.
CC SQ SEQUENCE 188 AA; 20451 MW; B43832FBC232CF4 CRC64;

Query Match 12.9%; Score 78.5; DB 1; Length 188;
Best Local Similarity 33.8%; Pred. No. 0.71;
Matches 26; Conservative 8; Mismatches 30; Indels 13; Gaps 5;

QY 32 GTGGAATTGNSCICRDSGTDSDSVTQOOAENSAVPTADRSQ--RDPVPRPRRG 89
DB 110 GRGASD--GDS-----DSGTDRSASQSPASQSRAPPTGQ--RQPARQAPQSPENFG 161
QY 90 PHE---PRRKKONVDGL 103
DB 162 DFNEIDPFPARPALDGI 178

RESULT 3
ID BAZB_HUMAN STANDARD; PRT, 1483 AA.
AC O95039; O95247; O95277;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bromodomain adjacent to zinc finger domain protein 1B (Williams-Beuren

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DE syndrome chromosome region 9 protein) (WBRS9) (Williams syndrome
DE transcription factor) (hWALP2).
GN BAZ1B OR WBSCR9 OR WBSC10 OR WSTRF.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA MEDLINE=9077764; PubMed=9858827;
RA Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
RT "Identification of the WBSCR9 gene, encoding a novel transcriptional
RT regulator, in the Williams-Beuren syndrome deletion at 7q11.23."
RL Cytogenet. Cell Genet. 82:238-246 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA MEDLINE=99047530; PubMed=9828126;
RA Lu X., Meng X., Morris C.A., Keating M.T.;
RA "A novel human gene, WSTRF, is deleted in Williams Syndrome."
RL Genomics 54:241-249 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=20130112; PubMed=10662543;
RX Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RL Genomics 63:40-45 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Minx P., Graves T., Duckels G., Harrison M., Waterston R.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=21977304; PubMed=11980720;
RX Bochenek L., Wade P.A., Varga-Melisz P.;
RT "WSRF-1SWI chromatin remodeling complex targets heterochromatic
RT replication foci."
RL EMO J. 21:2231-2241 (2002).
CC -1- FUNCTION: Forms a chromatin remodeling complex that mobilizes
CC nucleosomes and reconfigures irregular chromatin to a regular
CC nucleosomal array structure.
CC -1- SUBUNIT: Interacts with ISWI (imitation SWI protein) to form the
CC WSRF-1SWI chromatin remodeling complex (WICH).
CC -1- SUBCELLULAR LOCATION: Nuclear (potential). Accumulates in
CC pericentromeric heterochromatin during replication.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=G9UGO-1; Sequence=Displayed;
CC Name=2;
CC IsoId=G9UGO-2; Sequence=VSP_000552;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed with high levels of
CC expression in heart, brain, placenta, skeletal muscle and ovary.
CC -1- DEVELOPMENTAL STAGE: Expressed at equal levels in 19-23 weeks old
CC fetal tissues.
CC -1- DISEASE: Haploinsufficiency of BAZ1B may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC -1- SIMILARITY: Belongs to the WAL family.
CC -1- SIMILARITY: Contains 1 bromodomain.
CC -1- SIMILARITY: Contains 1 PBD domain.
CC -1- SIMILARITY: Contains 1 PHD-type zinc finger.
CC -1- SIMILARITY: Contains 1 WAC domain.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in positions 1031, 1042 and 1422.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 1478.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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DR EMBL; AF084791; AAC978675.1; ALT FRAM.  
DR EMBL; AF072810; AACC97879.1; ALT FRAM.  
DR EMBL; AB032253; BAA89210.1; ALT FRAM.  
DR EMBL; AC005074; AAAD4720.1; ALT SEQ.  
DR EMBL; AC005089; NOT_ANNOTATED_CDS.  
DR HSSP; Q92831; IBSI.  
DR TRANSFAC; TQ4145; -.  
DR Genew; HGNC; 961; BAZIB.  
DR MIM; 605681; -.  
DR GO; GO:0005634; C:nucleus; NAS.  
DR GO; GO:0003700; F:transcription factor activity; NAS.  
DR GO; GO:0008270; F:zinc ion binding; NAS.  
DR GO; GO:0006350; P:translation; NAS.  
DR InterPro; IPRO01487; Bromodomain.  
DR InterPro; IPRO04022; DDT_dom.  
DR InterPro; IPRO01965; Zn_f_PHD.  
DR Pfam; PF00439; bromodomain; 1.  
DR Pfam; PF00628; PHD; 1.  
DR PRINTS; PR00503; BROMODOMAIN.  
DR SMART; SMO02287; BROMO; 1.  
DR SMART; SMO0571; DDT; 1.  
DR SMART; SMO0249; PHD; 1.  
DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.  
DR PROSITE; PSS0014; BROMODOMAIN_2; 1.  
DR PROSITE; PSS0827; DDT; 1.  
DR PROSITE; PSS01359; ZN_PHD_1; 1.  
DR PROSITE; PSS0016; ZE_PHD_2; 1.  
KW transcription regulation; Bromodomain; Zinc-finger; Coiled coil;  
KW Nuclear protein; Alternative splicing; Williams-Beuren syndrome.
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FT FT NUCLEIC ACID  
FT DOMAIN  
FT ZN_FING 604 668  
FT ZN_FING 1184 1234  
FT DOMAIN 1356 1426  
FT DOMAIN 306 578  
FT DOMAIN 533 586  
FT LYS-RICH  
FT COILED COIL (POTENTIAL).  
FT COILED COIL (POTENTIAL).  
FT COILED COIL (POTENTIAL).  
FT COILED COIL (POTENTIAL).  
FT POLY-GLU  
FT MISSING (in isoform 2).  
FT VARSPLICC 660 663
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FT CONFLICT 14 14  
FT CONFLICT 22 22  
FT CONFLICT 136 136  
FT CONFLICT 191 191  
FT CONFLICT 298 298  
FT CONFLICT 823 823  
FT CONFLICT 1191 1191  
FT CONFLICT 1354 1354  
FT CONFLICT 1438 1438  
SEQUENCE 1483 AA; 170902 MW; 0CC146FB9B54261 CRC64;
```

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Query Match Similarity      12.8%; Score 78; DB 1; Length 1483;
Best Local Similarity      27.5%; Pred. No. 8;
Matches      22; Conservative      12; Mismatches      26; Indels      20; Gaps      3

QY      48 DDCGTDSDVDTQQQAENSVAVTATRTSGPRPVR-----PP-----RRRGPHHPRR    95
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1255 EDDSEDEEEEEEEDVEYAGLRFRPTIRKGSVTPPAARSGRRPGKKPHSTR    1314
          |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY       96 KK-----QNVDSGLDIT    107
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1315 SQPKAPVVDAAEVDLVLQT    1334
          |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
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ID MS2 PLAF1 STANDARD; PRT; 286 AA.
AC PS0496;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate 311).
OC Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=57265;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92178286; PubMed=1542312;
RA Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
RT "Two novel alleles within subfamilies of the merozoite surface
antigen 2 (MSA-2) of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 50:181-184(1992).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC CC
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CC -----
CC EMBL; M73809; AAA29697.1; -.
CC InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 262 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 263 286 HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
FT FT POLYMORPHIC REGION.
FT DOMAIN 44 212 POLY-THR.
FT FT 115 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 22 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 286 AA; 28844 MW; D1F4947CG68D5805 CRC64;

Query Match 12.3%; Score 75; DB 1; Length 286;
Best Local Similarity 34.6%; Pred. No. 2.5;
Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5

QY 32 GTGGA-----ATTMGSCICPDSDGDDBSV-----DT-----QQQAENSAPVADT 73
DB 147 GNGGQKKNQANKETONNSNV-QQDSQTKSNVPTQADTKSPTRQPDQANSA-FTAEQ 204
QY 74 RSQPRDPVPRPPRGGRPH 91
DB 205 TESPELQSAPEKGTGQH 222

RESULT 5
CCAA_HUMAN STANDARD; PRT; 2505 AA.
ID CCAA_HUMAN
AC 000555; P78511; Q12690; Q92690; Q99790; Q99791; Q99792;
AC Q99793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent P/Q-type calcium channel alpha-1A subunit (Calcium

```

QY	74	RSQPRDVKPPKRGKGFH	91
DB	205	TESPELOGAPENKGTGQH	222

RESULT 5

ID	CCAA_HUMAN	STANDARD	PRT: 2505 AA
AC	000555; P78510; P78511; Q16290; Q92650; Q99790; Q99791; Q99792;		
AC	Q99793;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Voltage-dependent P/Q-type calcium channel alpha-1A subunit (Calcium		

channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel
DE 1) (BI).
CN CACNA1A OR CACNA1A4 OR CAC4 OR CACN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
RC TISSUE=Neuron.
RX MEDLINE=99156614; PubMed=10049321;
RA Hans M., Urrutia A., Deal C., Ernst P.F., Stauderman K., Ellis S.B.,
RA Harold M.W., Johnson E.C., Williams M.B.,
RT "Structural elements in domain IV that influence biophysical and
RT pharmacological properties of human alpha1A-containing high-voltage-
RT activated calcium channels.";
RL Biophys. J. 76:1384-1400(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
RC TISSUE=Cerebellum;
RX MEDLINE=97053792; PubMed=8898206;
RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eljk R., Oefner P.J.,
RA Hoffman S.M.G., Lamerdin J.E., Mohrweiser H.W., Bulman D.E.,
RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
RA Ferrari M.D., Frants R.R.,
RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
RT mutations in the Ca²⁺ channel gene CACNA1A.";
RL Cell 87:543-552(1996).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=97414120; PubMed=8898170;
RA Zhubenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.,
RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
RT channel.";
RL Nat. Genet. 15:62-69(1997).
RN [4]
RP SEQUENCE OF 1233-1651 FROM N.A.
RX Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RX Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RX Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
RX Dangnan L., Poundsone P., Christensen M., Georgescu A., Ayala J.,
RX Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,
RX Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RX Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RX Kobayashi A., Olsen A.S., Carrano A.V.,
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 1693-1807 FROM N.A.
RC TISSUE=Lung carcinoma;
RX MEDLINE=95123449; PubMed=7823133;
RX Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.,
RT "Expression and antibody inhibition of P-type calcium channels in
RT human small-cell lung carcinoma cells.";
RL J. Neurosci. 15:274-283(1995).
RN [6]
RP SEQUENCE OF 2038-2258 FROM N.A.
RC TISSUE=Frontal cortex;
RX MEDLINE=96102310; PubMed=8525433;
RX Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
RX McIntis M.G., Ross C.A.,
RT "Characterization of cDNA clones containing CCA trinucleotide repeats
RT derived from human brain.";
RL Somat. Cell Mol. Genet. 21:279-284(1995).
RN -1-
RP FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. The isoform alpha-1A
CC gives rise to P and/or Q-type calcium currents. P/Q-type calcium
CC channels belong to the "high-voltage activated" (HVA) group and

are blocked by the funnel toxin (Ftx) and by the omega-egagotoxin-
CC IIVA (omega-Aga-IIVA). They are however insensitive to
CC dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTX-GVIA).
CC SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1-SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC SUBCELLULAR LOCATION: Integral membrane protein.
CC -1-
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=7;
CC Comment=Additional isoforms seem to exist;
CC Name=BI-1-GGCAG; Synonyms=1A-1;
CC IsoId=O00555-1; Sequence=Displayed;
CC Name=BI-1; Synonyms=1A-2;
CC IsoId=O00555-2; Sequence=VSP_000875;
CC Name=BI-1(V1);
CC IsoId=O00555-3; Sequence=VSP_000871, VSP_000875;
CC Name=BI-1(V1)-GGCAG;
CC IsoId=O00555-4; Sequence=VSP_000871;
CC Name=BI-1(V2);
CC IsoId=O00555-5; Sequence=VSP_000872;
CC Name=BI-1(V2)-GGCAG;
CC IsoId=O00555-6; Sequence=VSP_000872;
CC Name=BI-1(V2,V3);
CC IsoId=O00555-7; Sequence=VSP_000873, VSP_000874;
CC -1-
CC TISSUE SPECIFICITY: Brain specific; mainly found in cerebellum,
CC cerebral cortex, thalamus and hypothalamus. No expression in
CC heart, kidney, liver or muscle. Purkinje cells contain
CC predominantly P-type VSCC, the Q-type being a prominent calcium
CC current in cerebellar granule cells.
CC -1-
CC DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -1-
CC POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic: 6 to
CC 17 repeats in the normal population, expanded to about 21 to 30
CC repeats in spinocerebellar ataxia 6 (SCA6) patients. There seems
CC to be a correlation between the repeat number and earlier onset of
CC the disorder.
CC -1-
CC DISEASE: Defects in CACNA1A are the cause of spinocerebellar
CC ataxia type 6 (SCA6) [MIM:183086]. SCA6 is an autosomal dominant
CC disorder characterized by slowly progressive cerebellar ataxia of
CC the limbs and gait, dysarthria, nystagmus, and mild vibratory and
CC proprioceptive sensory loss. These symptoms are probably explained
CC by severe loss of cerebellar Purkinje cells. SCA6 is caused by
CC expansion of a CAG repeat in the coding region of CACNA1A.
CC -1-
CC DISEASE: Defects in CACNA1A are the cause of familial hemiplegic
CC migraine (FHM) [MIM:141500]; also known as migraine familial
CC hemiplegic 1 (FHM1). FHM, a rare autosomal dominant subtype of
CC migrating with aura, is associated with focal hemiparesis and, in
CC some families, progressive cerebellar atrophy.
CC -1-
CC DISEASE: Defects in CACNA1A are the cause of episodic ataxia type
CC 2 (EA-2) [MIM:108500]; also known as acetazolamide-responsive
CC hereditary paroxysmal cerebellar ataxia (APCA). This autosomal
CC dominant disorder is characterized by acetazolamide-responsive
CC attacks of cerebellar ataxia and migraine-like symptoms,
CC interictal nystagmus, and cerebellar atrophy.
CC -1-
CC SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, AF004884; AB061613.1; ..

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DR EMBL: AF004883; AAB61612.1; -
DR EMBL: X99897; CA68172.1; -
DR EMBL: Z68114; -; NOT_ANNOTATED_CDS.
DR EMBL: Z68115; -; NOT_ANNOTATED_CDS.
DR EMBL: U79666; AAB64179.1; -
DR EMBL: U79663; AAB49674.1; ALT_INIT.
DR EMBL: U79664; AAB49675.1; ALT_INIT.
DR EMBL: U79665; AAB49676.1; ALT_INIT.
DR EMBL: U79667; AAB49677.1; ALT_INIT.
DR EMBL: U79668; AAB49678.1; ALT_INIT.
DR EMBL: AC005305; AAC26839.1; -
DR EMBL: S76537; AAB35068.1; -
DR EMBL: U06702; -; NOT_ANNOTATED_CDS.
DR Genew; HGNC:1388; CACNA1A.
DR MIM; 601011; -
DR MIM; 183086; -
DR MIM; 141500; -
DR MIM; 108500; -
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR02077; Ca_channel_alpha.
DR InterPro; IPR002111; Cat_channel_Typl.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; Mchannell_nlg.
DR InterPro; IPR005448; PVDCCALPHAL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACNANEM.
DR PRINTS; PR01632; PVDCCALPHAL.
KW Calcium channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
KW Disease mutation; Triplet repeat expansion.
FT REPEAT 85 363
FT REPEAT 473 717
FT REPEAT 1231 1514
FT REPEAT 1551 1814
FT DOMAIN 1 98
FT TRANSMEM 99 117
FT DOMAIN 118 135
FT TRANSMEM 136 155
FT DOMAIN 156 167
FT TRANSMEM 168 185
FT DOMAIN 186 190
FT TRANSMEM 191 209
FT DOMAIN 210 228
FT TRANSMEM 229 248
Query Match 12.1%; Score 73.5; DB 1; Length 2505;
Best Local Similarity 24.2%; Pred. No. 41;
Matches 31; Conservative 9; Mismatches 39; Indels 49; Gaps 4;
QY 12 SRSIGGILLTLEHIAFLGTG-----ATTGNSC----- 44
DB 2247 SRSPSEG-----RHHMARQSSVSGSPAPISGISTPRRGRQLPQTSTRPHVSY 2201
QY 45 -ICRDSGTDDSVDTQQQAENSAY-----PTADTRSGPRDPVPPRRG 87
DB 2302 PVIRKAGSGPQQQQQQQQQQQAVARFGRATGPRRYPRPTAEPLAGDRPFGCHSSG 2361
QY 88 RGPHEPRR 95
DB 2362 RSPRMR 2369

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GN MS2.
OS Plasmodium falciparum (isolate thn / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=70151;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2090943;
RX MEDLINE=91218803; PubMed=2090943;
RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT "Sequence comparison of allelic forms of the Plasmodium falciparum
  merozoite surface antigen MS2."
RL Mol. Biochem. Parasitol. 43:211-220(1990).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
  erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
  (Potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  entities requires a license agreement (See http://www.ebi.ac.uk/announcements
  or send an email to license@ebi.ac.uk).
CC EMBL; M60189; AAA29689.1; -
DR InterPro; IPR001136; MS2_2.
DR Pfam; PF00985; MS2_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20
FT CHAIN 21 257
FT PROPEP 258 281
FT DOMAIN 44 207
FT DOMAIN 111 118
FT CARBOHYD 22 22
FT CARBOHYD 36 36
FT CARBOHYD 158 158
FT CARBOHYD 230 230
FT CARBOHYD 254 254
FT CARBOHYD 255 255
FT SEQUENCE 281 AA; 28992 MW; 50598AA42D64C8C64;
Query Match 12.0%; Score 73; DB 1; Length 281;
Best Local Similarity 35.8%; Pred. No. 4;
Matches 24; Conservative 6; Mismatches 25; Indels 12; Gaps 3;
QY 36 AATTGNSGICRDSGTDDSV-----DT-----QQQAENSAYPTADTRSGPRDPVPP 84
DB 152 ANETTONSNVQDSQTSNVFPPTQDADTKSPPTAOPBOAENSA-PTAQTESPELSAPE 210
QY 85 RRGRRGPH 91
DB 211 NKGTGQH 217

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RESULT 7
ID TGN1_MOUSE STANDARD; PRT; 353 AA.
AC 062313;
DT 15-MAR-2004 (Rel. 43; Created)
DT 15-MAR-2004 (Rel. 43; Last sequence update)
DE Trans-golgi network integral membrane protein 1 precursor (TGN38A).
GN TGN1 OR TGN1.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;

```

MEDLINE:95301533; PubMed:7540170;
 Kasai K., Takahashi S., Murakami K., Nakayama K.;
 "Strain-specific presence of two TGN38 isoforms and absence of TGN41
 in mouse.";
 J. Biol. Chem. 270:14471-14476(1995).
 [2]
 SEQUENCE FROM N.A.
 STRAIN: C57BL/6J; Tissue: Aorta, and Testis;
 MEDLINE:22354683; PubMed:12466851;
 Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikiido I., Otsu N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gogobori T.,
 Balderelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,
 Schriml L.M., Karapin A., Matsuda H., Batilov S., Beisel K.W.,
 Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazee K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.D., Pereira G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed U.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Sempke C.A., Seton M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang L.,
 Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
 Hirokawa K., Kishikawa T., Kono H., Nakamura M., Sakakura N., Sato K.,
 Shiraki T., Waki K., Kawai Y., Aizawa K., Aikawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shiragawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573(2002).
 [3]
 SEQUENCE FROM N.A.
 MEDLINE:22388257; PubMed:12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
 Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Tadin T.B., Toshyuki S., Carrinci P., Pange C.,
 Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millihy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Wooley K.C., Halse S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Botteffield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 [1]
 FUNCTION: May be involved in regulating membrane traffic to and
 from trans-Golgi network.
 [1]
 SUBCELLULAR LOCATION: Type I membrane protein. Primarily in trans-
 Golgi network. Cycles between the trans-Golgi network and the cell
 surface returning via endosomes (By similarity).
 [1]
 TISSUE SPECIFICITY: Widely expressed.
 [1]
 MISCELLANEOUS: Also found in strains BALB/c, C57BL/6 and DBA/2.
 [1]
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 CC -----
 CC EMBL: D50031; BAA08757.1; -
 CC DR EMBL: AK041302; BAC30896.1; -
 CC DR EMBL: AK076586; BAC36404.1; -
 CC DR EMBL: BC009143; AA009143.1; -
 CC DR PIR: B56940; B56940.
 CC DR MGI: MGI:105080; T9011.
 CC KW Signal: Transmembrane; Glycoprotein; Repeat; Golgi stack.
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 353
 CC FT
 CC FT DOMAIN 18 298
 CC FT TRANSMEM 299 319
 CC FT DOMAIN 320 353
 CC FT SITE 346 349
 CC FT DOMAIN 131 178
 CC FT REPEAT 131 138
 CC FT REPEAT 139 146
 CC FT REPEAT 147 154
 CC FT REPEAT 155 162
 CC FT REPEAT 163 170
 CC FT REPEAT 171 178
 CC FT CARBOHYD 110 110
 CC FT CARBOHYD 293 293
 CC SQ SEQUENCE 353 AA; 37848 MW; 95C340C2FA421B3 CRC4;
 Query Match 12.0%; Score 73; DB 1; Length 353;
 Best Local Similarity 30.5%; Pred. No. 5.1;
 Matches 16; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
 Oy 32 GTGAAATTGMSCCCPDSDTDSVDTQQQAENSAVPTADTSQRPDPYPRRGRGP 90
 Db 148 GDSGKPTFAGSNKATBEDDSKSTKTVLDKPTSKIS----PDTSTKTDVQVPRKQKP 202
 RESULT 8
 CAL3_HUMAN STANDARD; PRT; 1466 AA.
 ID CAL3_HUMAN Q15112; Created)
 AC P02461; Q15112; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(III) chain precursor.
 GN COL3A1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Skin fibroblast;
 RX MEDLINE=89350838; PubMed=2764886;
 RA Aikawa K., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
 Plokk-Kokko L.;
 "Structure of cDNA clones coding for the entire propeptide alpha 1 (III)
 chain of human type III procollagen. Differences in protein structure
 from type I procollagen and conservation of codon preferences.";
 J. Biochem. J. 260:509-516(1989).
 RN [2]
 RP SEQUENCE OF 149-1225 FROM N.A.
 RX MEDLINE=89386015; PubMed=2780304;
 RA Janeczko R.A., Ramirez F.;
 "Nucleotide and amino acid sequences of the entire human alpha 1
 (III) collagen.";
 Nucleic Acids Res. 17:6742-6742(1989).
 RN [3]
 RP SEQUENCE OF 168-398.
 RX MEDLINE=77134724; PubMed=557335;
 RA Seyer J.M., Kang A.H.;
 "Covalent structure of collagen: amino acid sequence of cyanogen

RT bromide peptides from the amino-terminal segment of type III collagen
 RT of human liver.";
 RL Biochemistry 16:1158-1164(1977).
 RN [4]
 RP REVISIONS.
 RA Seyer J.M.;
 RL Submitted (DEC-1977) to the PIR data bank.
 RN [5]
 RP SEQUENCE OF 399-727.
 RX MEDLINE=79000343; PubMed=687591;
 RA Seyer J.M., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of five
 RT consecutive CNBr peptides from type III collagen of human liver.";
 RL Biochemistry 17:3404-3411(1978).
 RN [6]
 RP SEQUENCE OF 728-964.
 RX MEDLINE=80198282; PubMed=6246925;
 RA Seyer J.M., Matnardi C., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of alpha 1
 RT (III)-CBs from type III collagen of human liver.";
 RL Biochemistry 19:1583-1589(1980).
 RN [7]
 RP SEQUENCE OF 950-1466 FROM N.A.
 RX MEDLINE=88189827; PubMed=3357782;
 RA Manco B.S., Daigleish R.;
 RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end,"
 RL Nucleic Acids Res. 16:2337-2337(1988).
 RN [8]
 RP REVISION TO 1184.
 RX MEDLINE=89098346; PubMed=3211760;
 RA Molynieux K., Daigleish R.;
 RT "Human type III collagen 'variant' is a cDNA cloning artefact.";
 RL Nucleic Acids Res. 16:11833-11833(1988).
 RN [9]
 RP SEQUENCE OF 1065-1466 FROM N.A.
 RX MEDLINE=85087944; PubMed=6096827;
 RA Loidl H.R., Brinker J.M., May M., Pahlajantemi T., Morrow S.,
 RA Rosenbloom J., Myers J.C.;
 RT "Molecular cloning and carboxyl-propeptide analysis of human type III
 RT procollagen.";
 RL Nucleic Acids Res. 12:9383-9394(1984).
 RN [10]
 RP SEQUENCE OF 965-1200.
 RX MEDLINE=81208139; PubMed=7016180;
 RA Seyer J.M., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of alpha
 RT 1(III)-CBs from type III collagen of human liver.";
 RL Biochemistry 20:2621-2627(1981).
 RN [11]
 RP SEQUENCE OF 1176-1466 FROM N.A.
 RX MEDLINE=85157600; PubMed=2579949;
 RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
 RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1
 RT (III) collagen. Partial characterization of the 3' end region of the
 RT gene.";
 RL J. Biol. Chem. 260:4357-4363(1985).
 RN [12]
 RP SEQUENCE OF 1161-1200 FROM N.A.
 RX MEDLINE=86187804; PubMed=3754462;
 RA Mikulin M., Daigleish R., Klueve-Beckerman B., Remnard S.I.,
 RA Tolstoev P., Brantly M., Crystal R.G.;
 RT "Human type III collagen gene expression is coordinately modulated
 RT with the type I collagen genes during fibroblast growth.";
 RL Biochemistry 25:1408-1413(1986).
 RN [13]
 RP SEQUENCE OF 1-170 FROM N.A.
 RP Tissue-Placenta;
 RX MEDLINE=88303360; PubMed=3405773;
 RA Toman D., Ricca G., de Crombrughe B.;
 RT "Nucleotide sequence of a cDNA coding for the amino-terminal region
 RT of human prepro alpha 1(III) collagen.";
 RL Nucleic Acids Res. 16:7201-7201(1988).
 RN [14]
 RP SEQUENCE OF 1-176 FROM N.A.
 RX MEDLINE=89378752; PubMed=2777083;
 RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
 RT "Cloning and analysis of the 5' portion of the human type-III
 RT procollagen gene (COL3A1).";
 RL Gene 78:255-265(1989).
 RN [15]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97255959; PubMed=9101290;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
 RT associated collagen (type IX), and network-forming collagen (type X)
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
 RL Hum. Mutat. 9:300-315(1997).
 RN [16]
 RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.
 RX MEDLINE=93293988; PubMed=8514866;
 RA Tromp G., Wu Y., Prockop D.J., Madhachari S.L., Kleinert C.,
 RA Earley J.J., Zhang J., Noerregaard O., Darling R.C., Abbott W.M.,
 RA Cole C.W., Jaakkola P., Rymaszewski M., Pearce W.H., Yao J.S.T.,
 RA Majamaa K., Smulens S.N., Galalica Z., Ferrell R.E., Jimenez S.A.,
 RA Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;
 RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations
 RT in the triple-helical domain of type III procollagen are an
 RT infrequent cause of aortic aneurysms.";
 RL J. Clin. Invest. 91:2539-2545(1993).
 RN [17]
 RP VARIANT THR-698.
 RX MEDLINE=91045136; PubMed=2235526;
 RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusari S.,
 RA Wu Y., Ganguly A., Prockop D.J.;
 RT "A mutation in the gene for type III procollagen (COL3A1) in a family
 RT with aortic aneurysms.";
 RL J. Clin. Invest. 86:1465-1473(1990).
 RN [18]
 RP VARIANT AORTIC ANEURYSM ARG-786.
 RX MEDLINE=91056445; PubMed=2243125;
 RA Kontusari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
 RT "A mutation in the gene for type III procollagen (COL3A1) in a family
 RT with aortic aneurysms.";
 RL J. Clin. Invest. 86:1465-1473(1990).
 RN [19]
 RP VARIANT EDS-IV ARG-828.
 RX MEDLINE=94016385; PubMed=8411057;
 RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
 RT "The substitution of glycine 661 by arginine in type III collagen
 RT produces mutant molecules with different thermal stabilities and
 RT causes Ehlers-Danlos syndrome type IV.";
 RL J. Med. Genet. 30:690-693(1993).
 RN [20]
 RP VARIANT EDS-IV SER-957.
 RX MEDLINE=89109135; PubMed=2492273;
 RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
 RT "A single base mutation that substitutes serine for glycine 790 of
 RT the alpha 1 (III) chain of type III procollagen exposes an arginine
 RT and causes Ehlers-Danlos syndrome IV.";
 RL J. Biol. Chem. 264:1349-1352(1989).
 RN [21]
 RP VARIANT EDS-IV VAL-960.
 RX MEDLINE=95268429; PubMed=7749417;
 RA Tromp G., de Paeppe A., Nuytink L., Madhachari S.L., Kuivaniemi H.;
 RT "Substitution of valine for glycine 793 in type III procollagen in
 RT Ehlers-Danlos syndrome type IV.";
 RL Hum. Mutat. 5:179-181(1995).
 RN [22]
 RP VARIANT EDS-IV GLU-1014.
 RX MEDLINE=92316511; PubMed=1352273;
 RA Richards A.J., Ward P.N., Narcisi P., Nicholas A.C., Lloyd J.C.,
 RA Pope F.M.;
 RT "A single base mutation in the gene for type III collagen (COL3A1)
 RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos
 RT syndrome type IV. An unaffected family member is mosaic for the
 RT mutation.";
 RL Hum. Genet. 89:414-418(1992).

RN [23]
 RP VARIANT EDS-IV ASP-1050.
 RX MEDLINE=90037070; PubMed=2808425;
 RA Tromp G., Kulivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
 RT "Single base mutation in the type III procollagen gene that converts
 RT the codon for glycine 883 to aspartate in a mild variant of
 RT Ehlers-Danlos syndrome IV.";
 RL J. Biol. Chem. 264:19313-19317(1989).
 RN [24]
 RP VARIANT EDS-IV VAL-1077.
 RX MEDLINE=91374480; PubMed=1895316;
 RA Richards A.J., Lloyd J.C., Ward P.N., de Paete A., Narcisi P.,
 RA Pope F.M.;
 RT "Characterisation of a glycine to valine substitution at amino acid
 RT position 910 of the triple helical region of type III collagen in a
 RT patient with Ehlers-Danlos syndrome type IV.";
 RL J. Med. Genet. 28:458-463(1991).
 RN [25]
 RP VARIANT EDS-IV GLU-1173.
 RX MEDLINE=93022543; PubMed=1357232;
 RA Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
 QY Query Match 12.0%; Score 73; DB 1; Length 1466;
 DB Best Local Similarity 28.8%; Pred. No. 25;
 DB Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7
 QY 16 GCGLLTLTEEH---TAHFVGTGCAATVMGNS-----CICRDSGT---DSD 55
 DB 8 GSWLLALHLPITIIAAGEAVAGGCSHLQGSVADRDVWKKPCGICVC--DSGSVLCDDI 65
 QY 56 V-DTQQQAENSAPV---TADTSQPRDPVPPRRGRGPHPR 94
 DB 66 ICDDDELDCPNPEIFGBCCAVCPQPPFAFRFP-NGQSPGPK 108
 RESULT 9
 MSAR2_PLAFC
 ID MSAR2_PLAFC STANDARD; PRT; 262 AA.
 AC Q99317;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merocyte surface antigen 2 precursor (MSA-2) (Allelic form 1).
 GN MSA2.
 OS Plasmodium falciparum (Isolate Camp / Malaysia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5835;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91218803; PubMed=2090943;
 RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
 RT "Sequence comparison of allelic forms of the Plasmodium falciparum
 RT merocyte surface antigen MSA2.";
 RL Wol. Biochem. Parasitol. 43:211-220(1990).
 RL -1- FUNCTION: May play a role in the merocyte attachment to the
 RL erythrocyte.
 CC SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
 CC
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 CC
 CC EMBL; M60186; AAA29687.1; -
 DR InterPro: IPR001136; MSA_2.
 DR Pfam: PF00985; MSA_2; 1.
 KW Malattia; Membrane; Glycoprotein; Antigen; Signal; Repeat; GPI-anchor; Merocyte.

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	238	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	239	262	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
FT	DOMAIN	44	188	POLYMORPHIC REGION.
FT	DOMAIN	91	98	POLY-THR.
FT	CARBOHYD	92	22	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	236	236	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	262 AA;	27374 MW;	72E0B2A315E9D154 CRC64;
Query Match		11.9%;	Score 72.5;	DB 1; Length 262;
Best Local Similarity		37.5%;	Pred. No. 4.1;	
Matches	24;	Conservative	6;	Mismatches 21; Indels 13; Gaps 4;
OY	39	TMNGSCCRDSDSGDDSV-----DT-----QQQQAENSAVFPADRRSOPRRVPPRRG	87	
DB	137	TQNNNSNV-QQDSQTKSVNPPTQADTKSPFAQPEQANSA-PIABQTESPELOSAPEKNG	194	
OY	88	RGPH 91		
DB	195	TGQH 198		
RESULT 10				
MSA2_PLAF7		STANDARD;	PRT;	272 AA.
ID	MSA2_PLAF7			
AC	PS0498;			
DT	01-OCT-1986	(Rel. 34, Created)		
DT	01-OCT-1986	(Rel. 34, Last sequence update)		
DT	01-OCT-1986	(Rel. 34, Last annotation update)		
DE	Merozoite surface antigen 2 precursor (MSA-2)	(45 kDa merozoite surface antigen).		
GN	MSA2.			
OS	Plasmodium falciparum (isolate JD7).			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.			
OK	NCBI_taxid=36329;			
RM	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90205972; PubMed=2181307;			
RA	Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J., Anders R.F.;			
RT	"Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodium falciparum."			
RL	Mol. Biochem. Parasitol. 39:227-234(1990).			
CC	-1- FUNCTION: May play a role in the merozoite attachment to the erythrocyte.			
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).			
CC	-1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.			
CC	-----			
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CC	or send an email to license@isb-sib.ch .			
CC	-----			
DR	EMBL; M28891; AAA29686.1; -			
DR	InterPro; IPR001136; MSA_2.			
DR	Pfam; PF000985; MSA_2; 1.			
KM	Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;			
KM	GPI-anchor; Merozoite.			
FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	248	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	249	272	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
FT	DOMAIN	44	198	POLYMORPHIC REGION.
FT	DOMAIN	95	108	POLY-THR.

Query Match 11.9%; Score 72.5; DB 1; Length 272;
 Best Local Similarity 37.5%; Pred. No. 4.3;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

Db 147 TONNSNV-QQDSQTSKSNVPTQADTSPTRAPQEAENSA-PTAEQTESPELQSAPEKNG 204

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQAENSAVPTADTRSQPRDPVPRPRG 87

MSA2_PLAF6 STANDARD; PRT; 274 AA.

AC P50497;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Merozoite surface antigen 2 precursor (MSA-2).
 GN MSA2.
 OS Plasmodium falciparum (isolate Kf1916).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=57269;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92178286; PubMed=1542312;
 RA Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
 RT "Two novel alleles within subfamilies of the merozoite surface
 antigen 2 (MSA-2) of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 50:181-184(1992).
 CC -1- FUNCTION: May play a role in the merozoite attachment to the
 erythrocyte.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 (Potential).
 CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M73810; AAA29698.1; -
 DR PIR: A45632; A45632.
 DR InterPro: IPR001136; MSA_2.
 DR Pfam: PF00985; MSA_2; 1.
 KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KM GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT CHAIN 21 250
 FT PROPEP 251 274
 FT
 FT DOMAIN 44 200
 FT DOMAIN 97 110
 FT CARBOHYD 22
 FT CARBOHYD 36
 FT CARBOHYD 151
 FT CARBOHYD 223
 FT CARBOHYD 248
 FT SEQUENCE 274 AA; 28367 MW; CEA832D766F743A2 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 274;
 Best Local Similarity 37.5%; Pred. No. 4.3;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

Db 149 TONNSNV-QQDSQTSKSNVPTQADTSPTRAPQEAENSA-PTAEQTESPELQSAPEKNG 206

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQAENSAVPTADTRSQPRDPVPRPRG 87

MSA2_PLAF6 STANDARD; PRT; 287 AA.

AC P19260;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 2)
 DE (Membrane protein p7).
 GN MSA2.
 OS Plasmodium falciparum (isolate FCR-3 / Gambia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90349616; PubMed=1696728;
 RA Elliott J.F., Albrecht G.R., Gilladoga A., Handunnetti S.M.,
 RA Neegaye J., Lallinger G., Minjas J.N., Howard R.J.;
 RT "Genes for Plasmodium falciparum surface antigens cloned by
 expression in COS cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91117264; PubMed=1990294;
 RA Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
 RA Ridley R., Scithe J.G., McBride J.S.;
 RT "Structural and antigenic polymorphism of the 35- to 48-kilodalton
 merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
 falciparum.";
 RL Mol. Cell. Biol. 11:963-971(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91218803; PubMed=2090943;
 RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
 RT "Sequence comparison of allelic forms of the Plasmodium falciparum
 merozoite surface antigen MSA2.";
 RL Mol. Biochem. Parasitol. 43:211-220(1990).
 CC -1- FUNCTION: May play a role in the merozoite attachment to the
 erythrocyte.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 (Potential).
 CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M28890; AAA29650.1; -
 DR EMBL: X53832; CA37429.1; -
 DR EMBL: M60188; AAA29688.1; -
 DR PIR: B39615; B39615.
 DR InterPro: IPR001136; MSA_2.
 DR Pfam: PF00985; MSA_2; 1.
 KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KM GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT POTENTIAL.

```

FT CHAIN 21 263 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 264 287 HYDROPHOBIC, REMOVED DURING MATURATION
FT 264 287 (BY SIMILARITY).
FT DOMAIN 44 213 POLYMORPHIC REGION.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 28555 MW; 368590DA917AF8 CRC64;

Query Match
Best Local Similarity 11.9%; Score 72.5; DB 1; Length 287;
Matches 24; Conservative 37.5%; Pred. No. 4.5; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQAENSAPVPTADTSQPRDPVPRRG 87
DB 162 TQNNSNV-QQDSQTSNVPTQDADTKSPVAPQEAENSA-PTAEQTESPELQSAPEKNG 219
QY 88 RGFH 91
DB 220 TQGH 223

RESULT 13
MSA2_PLAF1 STANDARD; PRT; 300 AA.
ID MSA2_PLAF1
AC Q03644;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate imr143).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57268;
RN [1]
RP MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
RT antigen 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
CC erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M59767; AAA29695.1; -
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20
FT CHAIN 21 276 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 277 300 HYDROPHOBIC, REMOVED DURING MATURATION
FT 277 300 (BY SIMILARITY).
FT DOMAIN 44 226 POLYMORPHIC REGION.
FT CARBOHYD 129 136 POLY-THR.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30101 MW; E416107747AA10D CRC64;

Query Match
11.9%; Score 72.5; DB 1; Length 300;
Matches 24; Conservative 37.5%; Pred. No. 4.8; Mismatches 21; Indels 13; Gaps 4;

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FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30131 MW; A01E17D36075D7D6 CRC64;

Query Match
Best Local Similarity 11.9%; Score 72.5; DB 1; Length 300;
Matches 24; Conservative 37.5%; Pred. No. 4.8; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQAENSAPVPTADTSQPRDPVPRRG 87
DB 175 TQNNSNV-QQDSQTSNVPTQDADTKSPVAPQEAENSA-PTAEQTESPELQSAPEKNG 232
QY 88 RGFH 91
DB 233 TQGH 236

RESULT 14
MSA2_PLAF2 STANDARD; PRT; 300 AA.
ID MSA2_PLAF2
AC Q03645;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate mad1 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70154;
RN [1]
RP MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
RT antigen 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
CC erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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DR EMBL; M59768; AAA29696.1; -
DR PIR; A39112; A39112.
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20
FT CHAIN 21 276 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 277 300 HYDROPHOBIC, REMOVED DURING MATURATION
FT 277 300 (BY SIMILARITY).
FT DOMAIN 44 226 POLYMORPHIC REGION.
FT CARBOHYD 129 136 POLY-THR.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30101 MW; E416107747AA10D CRC64;

Query Match
11.9%; Score 72.5; DB 1; Length 300;
Matches 24; Conservative 37.5%; Pred. No. 4.8; Mismatches 21; Indels 13; Gaps 4;

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: April 2, 2004, 09:39:06 / Search time 21 Seconds
(without alignments)
535,924 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGNAVFLASRLSGGLI.....QNVDDGLVDTLAVIRLVNDK 117

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85.5	14.0	290	T22161	hypothetical prote
2	79.5	13.0	612	T37181	thiamin biosynthes
3	75.5	12.4	900	B87957	protein Y106GD.7
4	75.5	12.4	948	T26417	hypothetical prote
5	75.5	12.3	248	S39310	merozoite surface
6	75.5	12.3	286	B45632	merozoite surface
7	73.5	12.1	91	PL0227	T-cell receptor be
8	73.5	12.0	1466	CGH77L	collagen alpha 1(I
9	73.5	12.0	2218	B84663	hypothetical prote
10	72.5	11.9	265	T05085	hypothetical prote
11	72.5	11.9	272	G71618	merozoite surface
12	72.5	11.9	274	A45632	merozoite 45K surf
13	72.5	11.9	287	B39615	merozoite 45K surf
14	72.5	11.9	300	A39112	merozoite 45K surf
15	72.5	11.9	302	A39615	merozoite 45K surf
16	72.5	11.9	347	B39112	hypothetical prote
17	72.5	11.9	458	S24457	hypothetical prote
18	72.5	11.8	707	T26218	hypothetical prote
19	72.5	11.8	1787	T20160	hypothetical prote
20	71.5	11.7	390	A47312	NS34 homolog - mur
21	71.5	11.7	310	T41982	hypothetical prote
22	71.5	11.7	22	T17401	transcription regu
23	70.5	11.6	1479	A35085	crithidia protein
24	70.5	11.5	113	T24164	hypothetical prote
25	69.5	11.4	279	T24164	hypothetical prote
26	69.5	11.4	318	C84651	hypothetical prote
27	69.5	11.4	773	F90537	11proprotein limor
28	69.5	11.3	261	AB5070	conserved hypotet
29	69.5	11.3	281	S26052	hypothetical prote

30	69	11.3	319	2	H98216	hypothetical prote
31	69	11.3	545	2	F84533	Mutator-like trans
32	69	11.3	775	2	B72074	hypothetical prote
33	69	11.3	775	2	C81594	hypothetical prote
34	69	11.3	775	2	D86549	hypothetical prote
35	69	11.3	876	2	PC2219	polypeptide - hepa
36	68.5	11.2	361	2	B56940	integral membrane
37	68.5	11.2	788	2	T25061	hypothetical prote
38	68	11.2	85	2	T07076	transcription fact
39	68	11.2	180	2	B45613	surface antigen FU
40	68	11.2	208	2	T46896	merozoite surface
41	68	11.2	272	2	T29446	hypothetical prote
42	68	11.2	351	2	T51513	hypothetical prote
43	68	11.2	445	2	A56043	steroid hormone re
44	68	11.2	482	2	A70963	hypothetical prote
45	68	11.2	504	2	S75134	cell division prot

ALIGNMENTS

RESULT 1

T22161 hypothetical protein F44D12.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T22161

R/Coles, L.

Submitted to the EMBL Data Library, December 1995

A/Reference number: Z19525

A/Accession: T22161

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-290 <ML>

A/Cross-references: EMBL:Z68298; PIDN:CAA92602.1; GSPDB:GN00022; CESP:F44D12.6

C/Genetics:

A/Map position: 4

A/Introns: 19/3; 154/2; 198/3

Query Match

Best Local Similarity 14.0%; Score 85.5; DB 2; Length 290;

Matches 27; Conservative 15; Mismatches 31; Indels 17; Gaps 5;

QY

24 EHHIAHFLGTGAATTGN-SCICRDSGTD-----DSVDYQQAENSAVPTADTRQOP 77

DB

154 DAHV-HMRETAGAFIRSDACRSKDGCDTIDSONSKEDRSKNSMPLSD----- 207

QY

78 RDVVRPPRRGRGPHBPRKKONVDGLVLD 107

DB

208 KKPDRKPO-----ETPRRSKORTPPPMPT 232

RESULT 2

T37181 thiamin biosynthesis protein thic SCQ11.11 [similarity] - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000

C/Accession: T37181

R/Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A/Reference number: Z21598

A/Accession: T37181

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-612 <SE>

A/Cross-references: EMBL:AI096823; PIDN:CAB46366.1; GSPDB:GN00070; SCQEDB:SCQ11.11

A/Experimental source: strain A3(2)

C/Genetics:

A/Map position: 4

A/Introns: 19/3; 154/2; 198/3

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Query Match      13.0%; Score 79; DB 2; Length 612;
Best Local Similarity 31.2%; Pred. No. 4.6;
Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

OY      39  TMGNSCICRDSG--TDSVDTQOQA-----ENSAPVTAATRSQPRDPVPR-----83
DB      60  TNGQSVTLVTDSGPTDPLVDTDRGLAPLENNWIIARGLTEHYAGRPVRFEDDG:KHT 119

OY      84  -FRGRG-----PHEPRRKQNDGLVLTAVIR 112
DB      120 SPRGLRMLDAVFGRPRQPRGRDGNVTLAVAR 155

RESULT 3
B87957 protein Y106G6D.7 (imported) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: B87957
R/Anonymous: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A15000; MUID:199069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_eleg
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: B87957
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-900 <STO>
A/Cross-references: GB:chr_I; PIND:CAA20980.1; PID:g3880680; GSPDB:GN00019; CESP:Y106G6D
C/Genetics:
A/Gene: Y106G6D.7
A/Map position: 1

Query Match      12.4%; Score 75.5; DB 2; Length 900;
Best Local Similarity 31.7%; Pred. No. 16;
Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

OY      50  SGTDDSDVTQOQAENSAPVTAATRSQPRDPVPR-----PFRGRGPHPRRKQ 98
DB      496 SHEDDKKSRSRWEN---TSPIRSPRSPLRDNDRSRSPRRRRRSRRREE 551

OY      99  NVD 101
DB      552 HTD 554

RESULT 4
T26417 hypothetical protein Y106G6D.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T26417
R/Murray, A.
Submitted to the EMBL Data Library, September 1998
A/Reference number: Z20211
A/Accession: T26417
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: DNA
A/Residues: 1-948 <ML>
A/Cross-references: EMBL:AJ031629; PIND:CAA20980.2; GSPDB:GN00019; CESP:Y106G6D.7
A/Experimental source: clone Y106G6D
C/Genetics:
A/Gene: CESP:Y106G6D.7
A/Map position: 1
A/Intons: 68/3; 160/3; 270/2; 624/2; 706/3; 888/3; 924/3

Query Match      12.4%; Score 75.5; DB 2; Length 948;
Best Local Similarity 31.7%; Pred. No. 16;
Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

OY      50  SGTDDSDVTQOQAENSAPVTAATRSQPRDPVPR-----PFRGRGPHPRRKQ 98
DB      496 SHEDDKKSRSRWEN---TSPIRSPRSPLRDNDRSRSPRRRRRSRRREE 551
```

```
DB      544 SHEDDKKSRSRWEN---TSPIRSPRSPLRDNDRSRSPRRRRRSRRREE 599
OY      99  NVD 101
DB      600 HTD 602

RESULT 5
S39310 merozoite surface antigen - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C/Accession: S39310
R/Ramasamy, R.; Kanasinghe, C.
Submitted to the EMBL Data Library, November 1993
A/Description: Cycle de DNA sequencing of a malaria parasite protein from infected blood
A/Reference number: S39310
A/Accession: S39310
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-278 <RAM>
A/Cross-references: EMBL:X76087; NID:g434996; PID:g836639
C/Superfamily: Epstein-Barr virus nuclear antigen
C/Keywords: surface antigen

Query Match      12.3%; Score 75; DB 2; Length 278;
Best Local Similarity 34.6%; Pred. No. 5;
Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

OY      32  GTGGA-----ATTGNSCICRDSGTDSV-----DT-----QOQAENSAPVTAAT 73
DB      139 GNGGVQKXQANKETQNNNV-QQDSQTSNVPPQTADTKSPAPQEAENSA-PTAQ 196

OY      74  RSQPRDPVPRRGRGPH 91
DB      197 TESPLOSAPEKKTGQH 214

RESULT 6
B45632 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C/Accession: B45632
R/Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A/Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A/Reference number: A45632; MUID:92178286; PMID:1542312
A/Accession: B45632
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <MAR>
A/Experimental source: isolate 311
A/Note: sequence extracted from NCBI backbone (NCBIN:85255, NCBI:P:85259)
C/Superfamily: Epstein-Barr virus nuclear antigen
C/Keywords: surface antigen

Query Match      12.3%; Score 75; DB 2; Length 286;
Best Local Similarity 34.6%; Pred. No. 5.1;
Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

OY      32  GTGGA-----ATTGNSCICRDSGTDSV-----DT-----QOQAENSAPVTAAT 73
DB      147 GNGGVQKXQANKETQNNNV-QQDSQTSNVPPQTADTKSPAPQEAENSA-PTAQ 204

OY      74  RSQPRDPVPRRGRGPH 91
DB      205 TESPLOSAPEKKTGQH 222

RESULT 7
P10227 T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)
C/Species: Homo sapiens
C/Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 01-Jun-1990
C/Accession: P10227
R/Barcellos, L.F.; Barcellos, L.F.; Barcellos, L.F.; Barcellos, L.F.
Submitted to the EMBL Data Library, June 1990
A/Description: T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)
A/Reference number: P10227
A/Accession: P10227
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-100 <PCR>
A/Cross-references: EMBL:P10227; NID:g434996; PID:g836639
C/Superfamily: T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)
C/Keywords: T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)
```

C/Species: Homo sapiens (man)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 30-May-1997
C/Accession: PLO0227
R/Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Ponnelt, D.N.
U. Exp. Med. 171, 221-230, 1990
A/Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.
A/Reference number: PLO225; MUID:90111615; PMID:1967999
A/Accession: PLO227
A/Molecule type: mRNA
A/Residues: 191 <LTY>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 12.1%; Score 73.5; DB 2; Length 91;
Best Local Similarity 34.1%; Pred. No. 2.1;
Matches 30; Conservative 8; Mismatches 21; Indels 29; Gaps 5;

OY 7 AVFLASRLGCGLLTIEHIAFLGGAATMGNSICRDSG-----TDDSV 56
DB 10 ALMYRQSLGQGL-----EPLTYF-----QGSN--APDKSLGSDRFAERTGSSV 53
OY 57 DT---QQQAENSAVPTADTRSPQPDV 81
DB 54 STLTIGTQGDSDAVYICASMPVPRDV 81

RESULT 8
CGHU7L
collagen alpha 1(III) chain precursor - human
N/Alternate names: procollagen alpha 1(III) chain
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C/Accession: S05272; S04642; PEO011; S01726; S04887; A90399; A94562; I51868; S59511; A90
R; Prockop, D.J.
submitted to the EMBL Data Library, February 1989
A/Reference number: S05272
A/Accession: S05272
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1240, 'V', 1242-1466 <PRC>
A/Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
R; Ala-Kokko, L.; Kontusarail, S.; Baldwin, C.T.; Kuitvanlent, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A/Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of huma
erences:
A/Reference number: S04642; MUID:89350838; PMID:2764886
A/Accession: S04642
A/Molecule type: mRNA
A/Residues: 1-1196 <ALA>
A/Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
R; Benson-Chanda, V.; Su, M.W.; Well, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A/Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
A/Reference number: PEO011; MUID:89378752; PMID:2777083
A/Accession: PEO011
A/Molecule type: DNA
A/Residues: 1-176 <BNA>
A/Cross-references: GB:M26939; NID:G180813; PIDN:AAA52040.1; PID:G180814
R; Toman, P.D.; Ricca, G.A.; de Crombrughe, B.
Nucleic Acids Res. 16, 7201, 1988
A/Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre
A/Reference number: S01726; MUID:88303360; PMID:3405773
A/Accession: S01726
A/Molecule type: mRNA
A/Residues: 1-170 <TOM>
A/Cross-references: EMBL:X07240; NID:G30060; PIDN:CAA30229.1; PID:G30061
A/Note: the authors translated the codon CAG for residue 154 as His
R; Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A/Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A/Reference number: S04887; MUID:89386015; PMID:2780304
A/Accession: S04887

A/Molecule type: mRNA
A/Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,
A/Cross-references: EMBL:X15332; NID:G29545; PIDN:CAA33387.1; PID:G930045
A/Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
R; Seyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977
A/Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A/Reference number: A90399; MUID:77134724; PMID:1557335
A/Accession: A90399
A/Molecule type: protein
A/Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEY1>
A/Experimental source: liver
A/Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R; Seyer, J.W.
submitted to the Atlas, December 1977
A/Reference number: A94562
A/Accession: A94562
A/Molecule type: protein
A/Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY2>
A/Experimental source: liver
A/Note: author submitted corrections to A90399
R; Milewicz, D.M.; Wiltz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A/Title: Parental somatic and germ-line mosaicism for a multilexon deletion with unusual
fingerprint.
A/Reference number: I51868; MUID:99304430; PMID:8317500
A/Accession: I51868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 186-194 <MIL>
A/Cross-references: GB:S62925; NID:G386425; PIDN:AD13937.1; PID:G4261637
R; Chodro, A.A.; Silence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A/Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A/Reference number: S59511; MUID:96067614; PMID:7487954
A/Accession: S59511
A/Molecule type: mRNA
A/Residues: 302-423 <CHI>
A/Cross-references: GB:S79877; NID:G1195576; PIDN:AA835615.1; PID:G1195577
R; Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
A/Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe
A/Reference number: A90414; MUID:79000343; PMID:687591
A/Accession: A90414
A/Molecule type: protein
A/Residues: 399-675, 'N', 677-727 <SEY3>
A/Experimental source: liver
R; Lee, B.; Vitale, E.; Superl-Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A/Title: G to T transversion at position +5 of a splice donor site causes skipping of th
A/Reference number: I55349; MUID:91161621; PMID:1672129
A/Accession: I55349
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 537-605 <LEB>
A/Cross-references: GB:M53312; NID:G180815; PIDN:AAA52041.1; PID:G180816
R; Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A/Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from cy
A/Reference number: A90438; MUID:80158282; PMID:6246925
A/Accession: A90438
A/Molecule type: protein
A/Residues: 728-895, 'A', 897-964 <SEY4>
A/Experimental source: liver
R; Cole, W.G.; Chiodo, A.A.; Lamanche, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan,
J. Biol. Chem. 265, 17070-17077, 1990
A/Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping and
A/Reference number: A38303; MUID:91009133; PMID:2145268
A/Accession: A38303
A/Molecule type: mRNA
A/Residues: 861-1015 <COL>
A/Cross-references: GB:U05617; GB:M55603; GB:M59227; NID:G180878; PIDN:AA859383.1; PID:G1
A/Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syndrome

R.Marko, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A>Title: Human pro alpha1(I)I collagen: cDNA sequence for the 3' end.
A/Reference number: S02119; MWID:88189827; PMID:3357782
A/Accession: S02119
A>Status: translation not shown
A/Molecule type: mRNA
A/Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
A/Cross-references: EMBL:X06700; NID:g30053; PDB:CAA2886.1; PID:g30054
R/Seyer, U.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
A/Reference number: A90446; MWID:81208139; PMID:7016180
A/Accession: A90446
A/Molecule type: protein
A/Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-
A/Experimental source: liver
R/Isoil, H.R.; Brinker, U.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
Nucleic Acids Res. 12, 9383-9394, 1984
A>Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
A/Reference number: A93551; MWID:85087944; PMID:6096827
A/Accession: A93551
A/Molecule type: mRNA
A/Residues: 1065-1155, 'P', 1157-1466 <LOI>
A/Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PDB:CAA25821.1
R/Miskulin, M.; Dalgleish, R.; Kiuv-Beckerman, B.; Renard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1408-1413, 1986
A>Title: Human type III collagen gene expression is coordinately modulated with the type
A/Reference number: 152393; MWID:86187804; PMID:3754462
A/Accession: 152393
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1161-1200 <MS>
A/Cross-references: GB:M13146; NID:g180415; PDB:AAA52003.1; PID:g180416
R/Emanuel, B.S.; Camitzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(I)I collagen. F
A/Reference number: 159025; MWID:85216505; PMID:3858826
A/Accession: 179359
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1165-1196
A/Cross-references: GB:M1134; NID:g180417; PDB:AAA52004.1; PID:g180418
R/Chu, M.L.; Wells, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
U. Biol. Chem. 260, 4357-4363, 1985
A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(I)I collagen. F
A/Reference number: A92516; MWID:85157600; PMID:2579949
A/Accession: A92516
A/Molecule type: DNA
A/Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>
A/Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GE
A/Experimental source: liver
A/Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given f
ation
C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit
3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently C
C/Genetic:
A/Gene: GDB:COL3A1
A/Cross-references: GDB:118729; OMIM:120180
A/Map position: 2q31-2q31
A/Intons: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A/Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
C/Complex: type III collagen is a homotrimer of monomers initially linked by disulfide b
er of their length, is formed with desmosine cross-links made from lysine and allysine
C/Function:
A/Description: structural component of extracellular fibrous polymer that maintains int
C/Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
C/Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; h
F:1-23/Domin: signal sequence #status predicted <SIG>
F:24-153/Domin: amino-terminal propeptide #status predicted <PRO>
F:31-91/Domin: von Willebrand factor type C repeat homology <WVC>
F:154-1221/Product: collagen alpha 1(I)I chain #status predicted <Mat>
F:154-167/Region: amino-terminal nonhelical telopeptide

F:168-1196/Region: helical
F:1091-1093/Region: cell attachment (R-G-D) motif
F:1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F:1122-1466/Domin: carboxyl-terminal propeptide #status predicted <CPR>
F:1238-1466/Domin: fibrillar collagen carboxyl-terminal homology <FCC>
F:153-154/Cleavage site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
F:151-1212/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predi
F:151-1212/Modified site: lysine (lys) #status predicted
F:263-284, 860, 977, 1106/Modified site: 5-hydroxylysine (lys) #status experimental
F:263/Binding site: carboxylate (lys) (covalent) #status experimental
F:584, 1094/Modified site: 5-hydroxylysine (lys) (partial) #status experimental
F:948-949/Cleavage site: Gly-Ile (collagenase) #status experimental
F:1106/Binding site: carboxylate (lys) (covalent) #status predicted

Query Match 12.0%; Score 73; DB 1; Length 1466;
Best Local Similarity 28.8%; Pred. No. 47;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;
QY 16 GGGLLTLESH---THTFGTAATTMNS-----CICRDSGT---DPS 55
DB 8 GSWLLTALHPHTITLQGEAVEGCSHLQSYADRVKWPBCQICV--DSGVLCDI 65
QY 56 V-DTQOQQAENSAYP---TADTRSQPRDPVPRPRGRGPRHPR 94
DB 66 ICDDQELDCNPFIRPFGECCAVCPQPTAPTRRP-NGQSPQGPX 108

RESULT 9
384683
hypochemical protein At2g28300 (Imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
A/Accession: B94683
R/Lin, X.; Kall, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talon, L.
euser, D.; Niekman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MWID:20083487; PMID:10617197
A/Accession: B94683
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2218 <STO>
A/Cross-references: GB:AB002093; NID:g4803953; PDB:AA22825.1; GSPDB:GN00139
C/Genetic:
A/Gene: At2g28300
A/Map position: 2

Query Match 12.0%; Score 73; DB 2; Length 2218;
Best Local Similarity 29.8%; Pred. No. 73;
Matches 29; Conservative 17; Mismatches 19; Indels 32; Gaps 7;
QY 45 ICRDSDS-----GTDDSV--DTQOQQAENSA---VPRADRS---QPRDPVRP--- 84
DB 49 LCQTESPDSPQKGSGESRLANDTSIVPENSDDLTPSPQATVQMEVPRQSHR 108

QY 85 -----RRGRGPRPRKKONVGLVDTLAVIRT 113
DB 109 LKERTQPIKGRG--RRKRTDKALTPVSL--AVSRT 141

RESULT 10
T05085
hypochemical protein T6X21.170 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
A/Accession: T05085
R/Beyan, M.; Rieger, M.; Muller-Auer, S.; Zipp, M.; Schaefer, M.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, February 1998
A/Reference number: Z15397
A/Accession: T05085
A/Molecule type: DNA

A/Residues: 1-265 <BBV>
 A/Cross-references: EMBL:AL02189
 A/Experimental source: Cultivar Columbia; BAC clone T6K21
 C/Genetics:
 A/Map position: 4
 A/Intons: 37/3; 59/2; 93/3; 163/1; 192/1
 A/Note: T6K21.170

Query Match 11.9%; Score 72.5; DB 2; Length 265;
 Best Local Similarity 23.5%; Pred. No. 8.4;
 Matches 36; Conservative 24; Mismatches 38; Indels 55; Gaps 9;

QY 2 IVFMAVFLASR--SLGGILLTLEHIAH-----FTG-----TGGA 37
 DB 112 VCIQYITLVAKDSAG-GSLVTFQTKVHEDYSKINTLVYTLARLKSPPDEIGGAK 170

QY 38 TTMGNS-----CICRDSGTDSDVDTCQQAENSAPVADRSQPRDPV-----RPPRRG 87
 DB 171 TGLSSSLIGTCHPCCKSVSKSVETEE-----VKQPNRLKRNAPVFIIRYIPNKG 224

QY 88 RGP-----HEPRRKQNVGVLDTLAVIRTLVD 116
 DB 225 RAPKGNHKKPR-----DRALITKRTMD 247

RESULT 11
 G71618
 merozoite surface antigen MSP-2 PFB0300C - malaria parasite (Plasmodium falciparum)
 C/Species: Plasmodium falciparum
 C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 17-Nov-2000

A/Accession: G71618; A44950
 R/Gardner, M.J.; Telcelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A/Reference number: A71600; MUID:99021743; PMID:9804551

A/Accession: G71618
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-272 <GAR>

A/Cross-references: GB:AE001385; GB:AE001362; NID:G3845143; PIDN:AAC71849.1; PID:G384514
 A/Experimental source: clone 3D7
 R/Smyle, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
 Mol. Biochem. Parasitol. 39, 227-234, 1990
 A/Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
 A/Reference number: A44950; MUID:90205972; PMID:2181307

A/Accession: A44950
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-54, 'T', '56-272 <SMY>

A/Cross-references: GB:M28891; NID:G160458; PID:G160459
 C/Genetics:
 A/Gene: PFB0300C
 C/Superfamily: Epstein-Barr virus nuclear antigen
 C/Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 272;
 Best Local Similarity 37.5%; Pred. No. 8.6;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TTMGNSCICRDSGTDSDV-----DT-----QQAENSAPVADTSQPRDPVPRRRG 87
 DB 147 TONNSNV-QQDSQTSKSNVPTQADTKSPTRAPQEAENSA-PTAEQTESPELQSAPEKNKG 204

QY 88 RGP 91
 DB 205 TQGH 208

RESULT 12
 A45632
 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
 C/Species: Plasmodium falciparum

C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: A45632
 R/Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
 Mol. Biochem. Parasitol. 50, 181-184, 1992
 A/Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
 A/Reference number: A45632; MUID:92178286; PMID:1542312

A/Contents: KF1916
 A/Accession: A45632
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-274 <MAR>
 A/Cross-references: GB:M73810; NID:G160484; PID:G160485
 A/Note: Sequence extracted from NCBI backbone (NCBI:85252, NCBI:85257)
 C/Superfamily: Epstein-Barr virus nuclear antigen
 C/Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 274;
 Best Local Similarity 37.5%; Pred. No. 8.7;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TTMGNSCICRDSGTDSDV-----DT-----QQAENSAPVADTSQPRDPVPRRRG 87
 DB 149 TONNSNV-QQDSQTSKSNVPTQADTKSPTRAPQEAENSA-PTAEQTESPELQSAPEKNKG 206

QY 88 RGP 91
 DB 207 TQGH 210

RESULT 13
 B39615
 merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum)
 N/Alternate names: membrane antigen pF7
 C/Species: Plasmodium falciparum
 C/Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 01-Dec-2000

A/Accession: B39615; A56018; A44950; A45613
 R/Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaife
 Mol. Cell. Biol. 11, 963-971, 1991
 A/Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
 A/Reference number: A39615; MUID:91117264; PMID:1990294

A/Accession: B39615
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-287 <FEN>
 A/Cross-references: EMBL:X53833

A/Note: clone T9-94
 R/Elloit, J.F.; Albrecht, G.R.; Gilladoga, A.; Handunnetti, S.M.; Neequaye, J.; Lallin
 Proc. Natl. Acad. Sci. U.S.A. 87, 6363-6367, 1990
 A/Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS ce
 A/Reference number: A36018; MUID:90349616; PMID:1696728

A/Accession: A36018
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-287 <ELL>

A/Cross-references: GB:M28890; NID:G160406; PID:G160407
 R/Smyle, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
 Mol. Biochem. Parasitol. 39, 227-234, 1990
 A/Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
 A/Reference number: A44950; MUID:90205972; PMID:2181307

A/Accession: B44950
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-186, 'R', 188-287 <SMY>

A/Cross-references: GB:M28892; NID:G160488; PID:G160489
 R/Fandeur, T.; Bonnefoy, S.; Mercereau-Pujalon, O.
 Mol. Biochem. Parasitol. 47, 167-178, 1991
 A/Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are genet
 A/Reference number: A45613; MUID:92049549; PMID:1944415

A/Accession: A45613
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 28, 'E', 30-186, 'R', 188-230, 'IH' <PAN>
 A/Experimental source: Uganda Palo Alto strain, merozoite

A>Note: sequence extracted from NCBI backbone (NCBIP:65035)
C:Superfamily: Epstein-Barr virus nuclear antigen
C:Keywords: membrane protein; surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 287;
Best Local Similarity 37.5%; Pred.No.9.1; 21; Indels 13; Gaps 4;
Matches 24; Conservative 6; Mismatches 21

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQQAENSAPVPTADRSQPRDPVPPRRG 87
Db 152 TQNNNSV-QQDSQTSNVPTQDADTKSPTAQPEQAENSA-PTAQTESPELQSAPEKNG 219

QY 88 RGPB 91
Db 220 TGOH 223

RESULT 14

A39112
merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (iso1
C:Species: Plasmodium falciparum
C>Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
C:Accession: A39112
R:Smyle, J.A.; Coppel, R.J.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; Ander
Proc Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991
A>Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.
A:Reference number: A39112; NUID:91156685; PMID:2000383
A:Accession: A39112
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <SMV>
A:Cross-references: GB:M59765
C:Superfamily: Epstein-Barr virus nuclear antigen
C:Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 300;
Best Local Similarity 37.5%; Pred.No.9.5;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQQAENSAPVPTADRSQPRDPVPPRRG 87
Db 175 TQNNNSV-QQDSQTSNVPTQDADTKSPTAQPEQAENSA-PTAQTESPELQSAPEKNG 232

QY 88 RGPB 91
Db 233 TGOH 236

RESULT 15

A39615
merozoite 45K surface antigen precursor (clone T9-96) - malaria parasite (Plasmodium fal
C:Species: Plasmodium falciparum
C>Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 17-Nov-2000
C:Accession: A39615; S13802
R:Penon, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaif
Mol. Cell. Biol. 11, 963-971, 1991
A>Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite su
A:Reference number: A39615; NUID:9117264; PMID:1990294
A:Accession: A39615
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-302 <PEN>
A:Cross-references: EMBL:X53832
C:Superfamily: Epstein-Barr virus nuclear antigen
C:Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 302;
Best Local Similarity 37.5%; Pred.No.9.6;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDSDV-----DT-----QQQQAENSAPVPTADRSQPRDPVPPRRG 87
Db 177 TQNNNSV-QQDSQTSNVPTQDADTKSPTAQPEQAENSA-PTAQTESPELQSAPEKNG 234

QY 88 RGPB 91
Db 235 TGOH 238

Search completed: April 2, 2004, 09:54:46
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:30:36 ; Search time 54 Seconds

(without alignments)
612.166 Million cell updates/sec

Title: US-10-066-500-9

Perfect score: 609
Sequence: 1 MIVFGMAVFLASRLSGGL.....QNVDELVIDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	117	4 AAB31180	AAB31180 Amino aci
2	609	100.0	117	6 ABO25151	ABO25151 Novel hum
3	609	100.0	117	6 ABU67269	ABU67269 Novel hum
4	609	100.0	117	6 ABU72037	ABU72037 Novel hum
5	609	100.0	117	6 ABU67138	ABU67138 Novel hum
6	609	100.0	117	6 ABU79780	ABU79780 Human sec
7	609	100.0	117	6 ABO33583	ABO33583 Novel hum
8	609	100.0	117	6 ADA47181	ADA47181 Human sec
9	609	100.0	117	7 ABO44436	ABO44436 Novel hum
10	609	100.0	117	7 ABO33460	ABO33460 Novel hum
11	609	100.0	117	7 ABO19838	ABO19838 Human sec
12	609	100.0	117	7 ADC17875	ADC17875 Human PRO
13	609	100.0	117	7 ADD11295	ADD11295 Human sec
14	609	100.0	117	7 ADD11255	ADD11255 Human sec
15	609	100.0	117	7 ADD70521	ADD70521 Human sec
16	609	100.0	117	7 ADD39598	ADD39598 Human sec
17	609	100.0	117	7 ADD70044	ADD70044 Human sec
18	609	100.0	117	7 ADD37048	ADD37048 Human sec
19	609	100.0	117	7 ADD38165	ADD38165 Human sec
20	609	100.0	117	7 ADD38121	ADD38121 Human sec
21	609	100.0	117	7 ADD38644	ADD38644 Human sec
22	609	100.0	117	7 ADD40075	ADD40075 Human sec
23	609	100.0	117	7 ADE50296	ADE50296 Human sec
24	609	100.0	117	7 ADE19908	ADE19908 Human sec
25	609	100.0	117	7 ADE49819	ADE49819 Human sec

ALIGNMENTS

26	609	100.0	117	7 ADE21377	ADe21377 Human sec
27	609	100.0	117	8 ADE41256	ADe41256 Human sec
28	609	100.0	117	8 ADE41104	ADe41104 Human sec
29	609	100.0	118	3 AAY99341	Aay99341 Human PRO
30	609	100.0	118	4 AAB66090	Aab66090 Protein o
31	609	100.0	118	5 ABB84819	Abb84819 Human PRO
32	609	100.0	118	5 ABB95425	Abb95425 Human ang
33	609	99.2	289	4 AAM25871	Aam25871 Human pro
34	604	99.2	427	2 AAY25761	Aay25761 Human sec
35	604	99.2	427	3 AAB32412	Aab32412 Human sec
36	604	99.2	436	3 AAB32411	Aab32411 Human sec
37	604	99.2	576	3 AAB32384	Aab32384 Human sec
38	604	99.2	576	4 AAB94297	Aab94297 Human pro
39	604	99.2	576	5 AAB64699	Aab64699 Human pro
40	85	14.0	961	6 ABU21450	Abu21450 Protein e
41	79.5	13.1	5002	4 ABB63723	Abb63723 Drosophi1
42	78	12.8	1527	2 AAW81172	Aaw81172 Human BAZ
43	78	12.8	1531	2 AAW81173	Aaw81173 Human BAZ
44	77	12.6	2618	4 ABG02135	Abg02135 Novel hum
45	77	12.6	2622	4 ABG06418	Abg06418 Novel hum

RESULT 1

AAB31180 standard; protein: 117 AA.

AAB31180;

20-APR-2001 (first entry)

Amino acid sequence of human polypeptide PRO444.

Human, secreted protein; transmembrane protein; PRO196; PRO444; PRO183; PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308; PRO1183; PRO1272; PRO1419; PRO1499; PRO170; PRO248; PRO353; PRO1118; PRO1600; PRO9940; PRO533; PRO187; PRO337; PRO1411; PRO4356; PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630; PRO3309; cell death; genetic disorder; transgenic animal; gene therapy.

Homo sapiens.

Location/Qualifiers

Key Peptide

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX (GENENTECH INC.)
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers J, Eaton DL;
XX Ferrera N, Fong S, Gao W, Gerber H, Gertsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kijavirij J, Mather JP, Napier MA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
XX Wood WI, Zhang Z;
XX WPI; 2001-050091/06.
XX N-PSDB; AAC86965.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
XX transmembrane polypeptide is useful for gene therapy and identification
XX of related polypeptides.
XX
XX Claim 12; Fig 4; 244pp; English.
XX
XX The present sequence represents a human secreted and transmembrane
XX polypeptide. The specification describes human polypeptides, designated
XX PRO1965, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO288,
XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO1170,
XX PRO348, PRO1361, PRO1318, PRO1600, PRO3940, PRO533, PRO301, PRO187,
XX PRO307, PRO1411, PRO3356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
XX PRO6004, PRO3350, PRO26309. The biological activity of cells
XX can be modulated with agents that bind to these polypeptides, resulting
XX in the death of the cells. The polynucleotides encoding these
XX polypeptides are useful in the recombinant production of the
XX polypeptides, as a hybridisation probe to screen libraries to isolate
XX homologous sequences, or to map the gene. They may also be used for
XX analysing genetic disorders, and to produce transgenic animals which are
XX useful for the development and screening of therapeutically useful
XX reagents. The polynucleotides can also be used in gene therapy e.g. to
XX replace a defective gene
XX
XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 609; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIVFGAVFLASRSIGQGLLTLEHIAFLGTGATMNSGCRDSDGSDSDVDDQ 60
DB 1 MIVFGAVFLASRSIGQGLLTLEHIAFLGTGATMNSGCRDSDGSDSDVDDQ 60
QY 61 QQAENSAVETADTRSGPRDPVPRPRGRGPHPRKKNQVDELVIDTLAVIRTLVDK 117
DB 61 QQAENSAVETADTRSGPRDPVPRPRGRGPHPRKKNQVDELVIDTLAVIRTLVDK 117
RESULT 2
ABO25151
ID ABO25151 standard; protein; 117 AA.
XX
XX ABO25151;
AC
XX
DT 05-SEP-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO444.
XX

KW Human; secreted and transmembrane protein; PRO; antidiabetic;
KW ophthalmological; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth.
XX
XX Homo sapiens.
XX
XX US2003040014-A1.
XX
XX 27-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066269.
XX
XX 26-AUG-1997; 97US-0056374P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063129P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.
XX 16-DEC-1997; 97US-0069694P.
XX 09-FEB-1998; 98US-0074086P.
XX 02-FEB-1998; 98US-0074292P.
XX 25-MAR-1998; 98US-0079294P.
XX 08-APR-1998; 98US-0081049P.
XX 14-JUL-1998; 98WO-US014552.
XX 10-AUG-1998; 98US-0095988P.
XX 18-AUG-1998; 98US-0097000P.
XX 09-SEP-1998; 98US-0099601P.
XX 10-SEP-1998; 98US-0099803P.
XX 10-SEP-1998; 98US-0099811P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 16-SEP-1998; 98WO-US019310.
XX 17-SEP-1998; 98US-0100858P.
XX 17-SEP-1998; 98WO-US019437.
XX 24-SEP-1998; 98US-0101922P.
XX 28-OCT-1998; 98US-0106032P.
XX 20-NOV-1998; 98US-0109304P.
XX 25-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025190.
XX 08-MAR-1999; 98WO-US025108.
XX 23-MAR-1999; 98US-0125778P.
XX 02-JUN-1999; 99WO-US012252.
XX 15-JUN-1999; 99US-0139695P.
XX 20-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145698P.
XX 17-AUG-1999; 99US-0149396P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021947.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99US-0028865P.
XX 07-DEC-1999; 99US-0169495P.
XX 20-DEC-1999; 99WO-US030999.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 09-MAR-2000; 2000WO-US006471.

PR 20-MAR-2000; 2000MO-US007377.
PR 30-MAR-2000; 2000MO-US008439.
PR 15-MAY-2000; 2000MO-US013358.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014541.
PR 02-JUN-2000; 2000MO-US015264.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023528.
PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gertlissen ME, Goddard A,
PI Godowski PJ, Gurney AL, Kijavini IJ, Macher JP, Napier MA, Pan Y,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX WPI; 2003-503396/47.
DR N-PSDB; ACD42316.
XX

PT New secreted and transmembrane PRO polypeptides, useful for treating
PT diabetes, retinal disorders and stimulating an immune response.
XX

PS Claim 12; Fig 4; 254pp; English.

XX The invention describes an isolated polypeptide (I) having at least 80 %
XX amino acid sequence identity to 30 secreted and transmembrane
XX polypeptides. PRO polypeptides are also useful for stimulating
XX hypertrophy of adult heart, for inhibiting vascular endothelial growth
XX factor stimulated proliferation of endothelial cells, stimulating
XX proliferation of stimulated T-lymphocytes and for inducing proliferation
XX of PD12 pancreatic ductal cells and are thus useful in the treatment of
XX disorders which involve protein secretion by the pancreas, including
XX diabetes. PRO polypeptides are useful for inducing vascular permeability
XX and in enhancing survival of retinal neurons cells and are thus useful
XX for the treatment of retinal disorders. PRO polypeptides are also useful
XX for stimulating an immune response and inducing inflammation by inducing
XX mononuclear cell and eosinophil infiltration at the site of infection of
XX an animal. The PRO polypeptides are further useful for inducing apoptosis
XX in endothelial cells for inhibiting neoplastic growth. This is the amino
XX acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX

SO Sequence 117 AA;

Query March 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pzcd. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRLSGGLTLLEHTAHFLGTGAATTWNSGICRDSGTDSDVDTQ 60
Db 1 MIVGMAVFLASRLSGGLTLLEHTAHFLGTGAATTWNSGICRDSGTDSDVDTQ 60
QY 61 QQAENSAPFTADTSSQPRDPYRPRRGGRGPRPKKQNDGLVLTAVIRTLVVK 117
Db 61 QQAENSAPFTADTSSQPRDPYRPRRGGRGPRPKKQNDGLVLTAVIRTLVVK 117

RESULT 3

ID AB067269 standard; protein. 117 AA.

XX AC AB067269;
XX

DT 28-MAY-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO444.

DE Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
XX PRO187; PRO337; PRO411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
XX PRO336; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
XX fibroblast growth factor receptor; cell death; chromosome mapping;
XX gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
XX obesity; diabetes; insulinemia; vascular permeability;
XX cardiac insufficiency disorder; immune response; hearing loss;
XX auditory hair cell regeneration; bone disorder; cartilage disorder;
XX sports injury; arthritis.

XX Homo sapiens.

XX US2003032063-A1.

XX 13-FEB-2003.

PP 01-FEB-2002; 2002US-00066494.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-0059115P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059588P.

XX 17-OCT-1997; 97US-0062855P.

XX 24-OCT-1997; 97US-0062816P.

XX 27-OCT-1997; 97US-0063082P.

XX 29-OCT-1997; 97US-0063332P.

XX 21-NOV-1997; 97US-0066364P.

XX 16-DEC-1997; 97US-0066949P.

XX 09-FEB-1998; 98US-0074066P.

XX 09-FEB-1998; 98US-0074092P.

XX 25-MAR-1998; 98US-0079294P.

XX 08-APR-1998; 98US-0081049P.

XX 10-AUG-1998; 98US-0095982P.

XX 18-AUG-1998; 98US-0097000P.

XX 09-SEP-1998; 98US-0099601P.

XX 10-SEP-1998; 98US-0099803P.

XX 10-SEP-1998; 98US-0099811P.

XX 10-SEP-1998; 98US-0099812P.

XX 14-SEP-1998; 98US-0103304P.

XX 16-SEP-1998; 98US-0103303P.

XX 17-SEP-1998; 98US-0100858P.

XX 17-SEP-1998; 98US-0101943P.

XX 24-SEP-1998; 98US-0101922P.

XX 28-OCT-1998; 98US-0106032P.

XX 20-NOV-1998; 98US-0109304P.

XX 20-NOV-1998; 98US-0109304P.

XX 25-NOV-1998; 98US-0109304P.

XX 01-DEC-1998; 98US-0109304P.

XX 08-MAR-1999; 99US-0125782P.

XX 23-MAR-1999; 99US-0125782P.

XX 02-JUN-1999; 99US-0136952P.

XX 15-JUN-1999; 99US-0136952P.

XX 20-JUL-1999; 99US-0145070P.

XX 26-JUL-1999; 99US-0145070P.

XX 17-AUG-1999; 99US-0149396P.

XX 01-SEP-1999; 99US-0200211P.

XX 08-SEP-1999; 99US-0200259P.

XX 15-SEP-1999; 99US-0201090P.

XX 15-SEP-1999; 99US-0201090P.

XX 30-NOV-1999; 99US-0202831P.

XX 01-DEC-1999; 99US-0202831P.

XX 02-DEC-1999; 99US-0202831P.

XX 07-DEC-1999; 99US-0169495P.

XX 20-DEC-1999; 99US-0169495P.

XX 05-JAN-2000; 2000US-0000219P.

XX 18-FEB-2000; 2000US-0000341P.

XX 18-FEB-2000; 2000US-0000342P.

PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 09-MAR-2000; 2000MO-US006471.
PR 20-MAR-2000; 2000MO-US007377.
PR 30-MAR-2000; 2000MO-US008439.
PR 15-MAY-2000; 2000MO-US013358.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023528.
PR 01-DEC-2000; 2000MO-US02678.
PR 28-FEB-2001; 2001MO-US006520.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUL-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gertsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Kijavini IU, Mather JP, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
XX Wood WL, Zhang Z;
XX WPI; 2003-341964/32.
DR N-PSDB; ACA04925.
XX
XX Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
PT polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping.
XX
XX Claim 12; Fig 4; 255pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO41, fibroblast growth
CC factor receptor (FGFR-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptide. The bioactive molecule causes cell
CC death. (II) is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ad is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or anti-
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This is the amino acid
CC sequence of a novel human secreted and transmembrane polypeptide
CC associated oligonucleotide
XX
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 609; DB 6; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2e-63; 0; Indels 0; Gaps 0;
XX Matches 117; Conservative 0; Mismatches 0;
XX
XX 1 MIVFGNAVFLASRLSGILLTLEHIAHFLGTGAATTGSCICRDSGTDSDVDTQQ 60
XX 1 MIVFGNAVFLASRLSGILLTLEHIAHFLGTGAATTGSCICRDSGTDSDVDTQQ 60
XX 1 MIVFGNAVFLASRLSGILLTLEHIAHFLGTGAATTGSCICRDSGTDSDVDTQQ 60

QY 61 QQAENSAVPTADTRSGPRDPVPPRRGRGPHRRKKQNVGLVLTAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSGPRDPVPPRRGRGPHRRKKQNVGLVLTAVIRTLVDK 117
RESULT 4
ABU72037 standard; protein; 117 AA.
ID ABU72037;
AC ABU72037;
XX
XX 11-JUN-2003 (first entry).
XX
XX Novel human secreted and transmembrane protein PRO444.
DE
XX Human; secreted and transmembrane polypeptide; PRO;
KM fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KM PRO1411; PRO10096; PRO246; PRO6307; FGFR-3; FGFR-4; FGFR-1;
KM FGFR-2; PRO6004; PRO4356; PRO265; PRO951; bioactive molecule;
KM toxin; radiolabel; antibody; cell death; chromosome mapping;
KM gene mapping; transgenic animal; knockout animal; gene therapy;
KM tissue typing.
XX
XX Homo sapiens.
OS
XX US2002177165-A1.
XX 28-NOV-2002.
XX
XX 01-FEB-2002; 2002US-00066500.
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.
XX 16-DEC-1997; 97US-0069694P.
XX 09-FEB-1998; 98US-0074086P.
XX 09-FEB-1998; 98US-0074092P.
XX 25-MAR-1998; 98US-0079294P.
XX 08-APR-1998; 98US-0081049P.
XX 14-JUL-1998; 98MO-US014552.
XX 10-AUG-1998; 98US-0095988P.
XX 18-AUG-1998; 98US-0097000P.
XX 09-SEP-1998; 98US-0099601P.
XX 10-SEP-1998; 98US-0099803P.
XX 10-SEP-1998; 98US-0099811P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98MO-US018824.
XX 10-SEP-1998; 98MO-US019093.
XX 14-SEP-1998; 98MO-US019330.
XX 16-SEP-1998; 98MO-US019330.
XX 17-SEP-1998; 98MO-US019437.
XX 17-SEP-1998; 98MO-US019437.
XX 24-SEP-1998; 98US-0101922P.
XX 28-OCT-1998; 98US-0106032P.
XX 20-NOV-1998; 98US-0109304P.
XX 20-NOV-1998; 98MO-US024855.
XX 25-NOV-1998; 98MO-US025190.
XX 01-DEC-1998; 98MO-US025108.
XX 08-MAR-1999; 99MO-US005028.
XX 23-MAR-1999; 99US-0125778P.
XX 02-JUN-1999; 99MO-US012252.
XX 15-JUN-1999; 99US-0136695P.
XX 20-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145668P.
XX 17-AUG-1999; 99US-0149336P.

PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
XX Ferrera N, Fong S, Gao W, Gerber H, Gerlitsen ME, Goddard A,
XX Godowski PJ, Gunney AL, Kijavitt ID, Mather JP, Napier MA, Pan J,
XX Paoni NF, Roy MA, Stewart TM, Tumas D, Watanabe CK, Williams PM,
XX Wood WL, Zhang Z;
XX WPI; 2003-328482/31.
XX N-PSDB; ACA60455.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
XX activity of cell expressing the polypeptide, for identifying agonists or
XX antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 12; Fig 4; 254P; English.
XX
XX The invention describes an isolated, secreted and transmembrane
XX polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
XX (1), (i) is useful for detecting PRO33, PRO301, PRO187, PRO337, PRO411,
XX PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
XX (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6304, PRO335, PRO630, PRO295 or
XX PRO951 polypeptide, and for linking a bioactive molecule to a cell
XX expressing the above polypeptides. The bioactive molecule, a toxin,
XX radiolabel or an antibody, causes cell death. PRO is useful in assays to
XX identify other proteins or molecules involved in binding interaction. The
XX polynucleotide (II) encoding (I) is useful in chromosome and gene
XX mapping, in generation of antisense RNA and DNA, for generating
XX transgenic animals or knockout animals which in turn are useful in the
XX development and screening of therapeutically useful reagents, to
XX construct hybridisation probes for mapping the gene which encodes the PRO
XX and for the genetic analysis of individuals with genetic disorders, in
XX gene therapy, for chromosome identification and as a chromosome marker.
XX (I) and (II) are useful for tissue typing. This is the amino acid
XX sequence of a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 117 AA;
XX
XX

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 26-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB
QY 1 MIVEGMAVFLASRLSGQLLTLEHIAHFLGTGGAATTMGNSCICRDSGTDSDVDTQQ 60
1 MIVEGMAVFLASRLSGQLLTLEHIAHFLGTGGAATTMGNSCICRDSGTDSDVDTQQ 60
QY 61 QQAENSAPFTADTSQPPDPFRPPRRGGRGPRRRKQNVGVLDTLAVIRTLVDR 117
61 QQAENSAPFTADTSQPPDPFRPPRRGGRGPRRRKQNVGVLDTLAVIRTLVDR 117
DB
RESULT 5
ABU67138
ID ABU67138 standard; protein, 117 AA.
XX
XX ABU67138;
AC
XX
XX 28-MAY-2003 (first entry)
DT
XX
XX
DE Novel human secreted and transmembrane protein PRO444.
XX
XX
XX Secreted and transmembrane polypeptide, PRO polypeptide, PRO301;
XX PRO187, PRO337, PRO411, PRO10096, PRO246, PRO6307, PRO6003, PRO6004;
XX PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
XX fibroblast growth factor receptor; cell death; chromosome mapping;
XX gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
XX obesity; diabetes; insulinemia; vascular permeability;
XX cardiac insufficiency disorder; immune response; hearing loss;
XX auditory hair cell regeneration; bone disorder; cartilage disorder;
XX sports injury; arthritis.
XX
XX Homo sapiens.
OS
XX
XX
XX US2003032062-A1.
XX
XX
XX 13-FEB-2003.
XX
XX
XX 01-FEB-2002; 2002US-00066273.
XX
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0058263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062858P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0063640P.
XX 25-NOV-1997; 97US-0066840P.
XX 16-DEC-1997; 97US-0069694P.
XX 09-FEB-1998; 97US-0074086P.
XX 09-FEB-1998; 97US-0074092P.
XX 25-MAR-1998; 97US-0075294P.
XX 08-APR-1998; 97US-0081049P.
XX 14-JUL-1998; 97US-0081455P.
XX 10-AUG-1998; 97US-0095958P.
XX 18-AUG-1998; 97US-0097000P.
XX 09-SEP-1998; 97US-0099601P.
XX 10-SEP-1998; 97US-0099803P.
XX 10-SEP-1998; 97US-0099811P.
XX 10-SEP-1998; 97US-0099812P.
XX 10-SEP-1998; 97US-0099812P.
XX 14-SEP-1998; 97US-0099812P.
XX 14-SEP-1998; 97US-0099812P.
XX 16-SEP-1998; 97US-0099812P.
XX 16-SEP-1998; 97US-0099812P.
XX 17-SEP-1998; 97US-0099812P.
XX 17-SEP-1998; 97US-0099812P.
XX 24-SEP-1998; 97US-0099812P.
XX 28-OCT-1998; 97US-0099812P.
XX 20-NOV-1998; 97US-0099812P.
XX 20-NOV-1998; 97US-0099812P.

PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005078.
 PR 23-MAR-1999; 99WO-US012578P.
 PR 02-JUN-1999; 99WO-US012522.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004414.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017444.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desroyers L, Eaton DL,
 PI Ferrara N, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J,
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WI, Zhang Z;
 XX
 DR WFI, 2003-341963/32.
 DR N-PSDB; ACA04445.
 XX
 PT New secreted and transmembrane polypeptide for modulating biological
 PT activity of a cell expressing the polypeptide, identifying agonists or
 PT antagonists of the polypeptide, and as molecular weight markers.
 XX
 PS Claim 12; Fig 4; 254pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO3356, PRO2630, PRO265, PRO341, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptide. The bioactive molecule causes cell
 CC death. (II) is useful as hybridisation probe, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This is the amino acid
 CC sequence of a novel human secreted and transmembrane polypeptide
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTFGNVAVPLASRLGQGLTLLEHIAHFLTGGAATMGNSCTCRDSDGTRDSDVDTQ 60
 DB 1 MTFGNVAVPLASRLGQGLTLLEHIAHFLTGGAATMGNSCTCRDSDGTRDSDVDTQ 60
 QY 61 QCAENSAVPTADTRSQPRDPVPPRRGRGPHPRKKQNVDTLVITLAVITLVYDK 117
 DB 61 QCAENSAVPTADTRSQPRDPVPPRRGRGPHPRKKQNVDTLVITLAVITLVYDK 117
 RESULT 6
 ABUT9780 ID ABUT9780 standard; protein; 117 AA.
 XX
 AC ABUT9780;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO444.
 XX
 KW Human secreted protein; transmembrane protein; PRO; genetic disorder;
 XX gene therapy.
 KW Homo sapiens.
 OS
 XX US2003032057-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 15-NOV-2001; 2001US-00002796.
 XX
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 19-SEP-1997; 97US-0059588P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 24-OCT-1997; 97US-0062816P.
 XX 24-OCT-1997; 97US-0063082P.
 XX 27-OCT-1997; 97US-0063329P.
 XX 29-OCT-1997; 97US-0063733P.
 XX 21-NOV-1997; 97US-0066364P.
 XX 25-NOV-1997; 97US-0066840P.
 XX 16-DEC-1997; 97US-0069694P.
 XX 09-FEB-1998; 98US-0074086P.
 XX 09-FEB-1998; 98US-0074092P.
 XX 25-MAR-1998; 98US-0079284P.
 XX 08-APR-1998; 98US-0081049P.
 XX 14-JUL-1998; 98WO-US014552.
 XX 10-AUG-1998; 98US-0095998P.
 XX 18-AUG-1998; 98US-0097000P.
 XX 09-SEP-1998; 98US-0099601P.
 XX 10-SEP-1998; 98US-0099803P.
 XX 10-SEP-1998; 98US-0099811P.
 XX 10-SEP-1998; 98US-0099812P.
 XX 10-SEP-1998; 98WO-US018824.
 XX 14-SEP-1998; 98WO-US019093.
 XX 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98MO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98MO-US024655.
 PR 25-NOV-1998; 98MO-US025190.
 PR 01-DEC-1998; 98MO-US025108.
 PR 08-MAR-1999; 99MO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99MO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 08-SEP-1999; 99MO-US020594.
 PR 15-SEP-1999; 99MO-US021090.
 PR 15-SEP-1999; 99MO-US021547.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 02-DEC-1999; 99MO-US028565.
 PR 07-DEC-1999; 99US-0169455P.
 PR 20-DEC-1999; 99MO-US030999.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 09-MAR-2000; 2000MO-US006471.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 15-MAY-2000; 2000MO-US013358.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 PI Perreira N, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A,
 PI Goddardi EJ, Gurney AL, Kijavrin IU, Mather JP, Nephler MA, Pan J,
 PI Paotii NF, Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WT, Zhang Z;
 PI XX
 DR WPI; 2003-341960/32.
 DR N-PSDB; ACA65586.
 XX
 PT Novel, secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 12; Fig 4; 255PP; English.
 CC The invention relates to an isolated, secreted/transmembrane polypeptide,
 CC termed PRO polypeptide, having at least 80% sequence identity to a
 CC sequence selected from any one of the 37 sequences appearing as ABU79779
 CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 CC under any one of the ATCC numbers given in the specification. Also
 CC included are an isolated nucleic acid molecule having at least 80%
 CC sequence identity to a sequence selected from any one of the 37 cDNA

CC sequences defined in the specification (or encoding the mature PRO
 CC protein or a PRO protein extracellular domain), a PRO expression vector,
 CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
 CC antibodies and a method for linking a bioactive molecule to a cell
 CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 CC radiolabel or an antibody and causes the death of the cell. PRO or the
 CC antibody is useful for modulating at least one biological activity of
 CC cell expressing the above polypeptides. PRO is useful for identifying
 CC agonists or antagonists of PRO, for preparing a variant of PRO, as
 CC molecular weight markers for protein electrophoresis purpose and PRO
 CC nucleic acid is useful for recombinantly expressing those markers. PRO is
 CC also useful as therapeutic agent. PRO is useful in assays to identify
 CC other proteins or molecules involved in binding interaction. PRO nucleic
 CC acid is useful as hybridisation probes, in the preparation of PRO
 CC in generation of antisense RNA and DNA, in the preparation of PRO
 CC polypeptide, in gene therapy, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, to construct hybridisation
 CC probes for mapping the gene which encodes the PRO and for the genetic
 CC analysis of individuals with genetic disorders, for chromosome
 CC identification, as a chromosome marker, and for generating probes for
 CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 CC Western analysis. The antibody is useful in diagnostic assays for PRO,
 CC e.g. detecting its expression in specific cells, tissues or serum, for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. PRO or Ab is useful for the preparation of medicament for
 CC treating conditions which is responsive to the PRO polypeptide or anti-
 CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 CC present sequence encodes a PRO polypeptide
 CC XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRSLGQGLLTLEHIAHFLTGAAATTMGNSCCIRDDSGTDSVDTQQ 60
 Db 1 MIVFGWAVFLASRSLGQGLLTLEHIAHFLTGAAATTMGNSCCIRDDSGTDSVDTQQ 60
 QY 61 QQAENSAVPTADTRSPDPVAPRRGRGPHPRKKNQVDTLAVITLVYDK 117
 Db 61 QQAENSAVPTADTRSPDPVAPRRGRGPHPRKKNQVDTLAVITLVYDK 117

RESULT 7
 ABO33583 standard; protein; 117 AA.

ABO33583;

DT 17-SEP-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO444.
 DE
 XX

KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumor;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis.
 KW XX

OS Homo sapiens.

XX US2003073130-A1.

XX 17-APR-2003.

PD
 XX

PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US016692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart RA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX WPI; 2003-585293/55.
DR N-PSDB; ACDE8242.
XX
PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 char modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 28-63; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;

QY 1 MIVFGNAVFLASRLGGGLLTLEHIAHPIGTGAATTGNSGICRDSGTFDSDVTQO 60
DB 1 MIVFGNAVFLASRLGGGLLTLEHIAHPIGTGAATTGNSGICRDSGTFDSDVTQO 60
QY 61 QQAENSAVPTADTRSGPRDPRPRGRGCPHEPRKKQNVGILVDTLAVIRTLVDK 117
DB 61 QQAENSAVPTADTRSGPRDPRPRGRGCPHEPRKKQNVGILVDTLAVIRTLVDK 117

RESULT 8
ADA47181
ID ADA47181 standard; protein; 117 AA.
XX
AC ADA47181;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO444.
XX
XX human; secreted protein; transmembrane protein; PRO; VEGF inhibitor;
XX vascular endothelial growth factor; endothelial cell proliferation;
XX T-lymphocyte proliferation; endothelial cell apoptosis;
XX C-fos stimulation; pancreatic beta cell differentiation;
XX chondrocyte proliferation; glucose uptake; free fatty acid; FFA uptake;
XX tissue typing.
XX
XX Homo sapiens.
XX OS
XX US2003044844-A1.
XX
PN 06-MAR-2003.
XX
XX 01-FEB-2002; 2002US-00066211.
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062815P.

PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063232P.
PR 29-OCT-1997; 97US-0063733P.
PR 25-NOV-1997; 97US-006364P.
PR 16-DEC-1997; 97US-0066840P.
PR 09-FEB-1998; 97US-0069694P.
PR 09-FEB-1998; 97US-0074086P.
PR 25-MAR-1998; 97US-0079292P.
PR 08-APR-1998; 97US-0081049P.
PR 14-JUL-1998; 97US-0081452P.
PR 10-AUG-1998; 97US-0095998P.
PR 18-AUG-1998; 97US-0097000P.
PR 09-SEP-1998; 97US-0099601P.
PR 10-SEP-1998; 97US-0099803P.
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PR 10-SEP-1998; 97US-0099812P.
PR 10-SEP-1998; 97US-0099812P.
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PR 16-SEP-1998; 97US-0100858P.
PR 17-SEP-1998; 97US-0100858P.
PR 24-SEP-1998; 97US-0101933P.
PR 28-OCT-1998; 97US-0106032P.
PR 20-NOV-1998; 97US-0109304P.
PR 20-NOV-1998; 97US-0109304P.
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PR 01-DEC-1998; 97US-0109304P.
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PR 26-JUL-1999; 97US-0145698P.
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PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 22-FEB-2000; 2000MO-US004342.
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PR 02-MAR-2000; 2000MO-US005601.
PR 09-MAR-2000; 2000MO-US005601.
PR 20-MAR-2000; 2000MO-US005601.
PR 30-MAR-2000; 2000MO-US005601.
PR 30-MAR-2000; 2000MO-US005601.
PR 15-MAY-2000; 2000MO-US013358.
PR 15-MAY-2000; 2000MO-US013358.
PR 22-MAY-2000; 2000MO-US013705.
PR 30-MAY-2000; 2000MO-US014942.
PR 02-JUN-2000; 2000MO-US014942.
PR 11-AUG-2000; 2000MO-US020203.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023522.
PR 01-DEC-2000; 2000MO-US023522.
PR 28-FEB-2001; 2001MO-US006520.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 09-JUL-2001; 2001MO-US021066.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI

PI Ferrera N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gunney AL, Kijavitt IT, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy NA, Stewart IA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
XX MPI; 2003-615775/58.
DR N-PSDB; ADA47180.

PT Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
PT inducing redifferentiation and/or proliferation of chondrocytes, and for
PT inducing glucose or free fatty acid uptake by skeletal muscle cells.

PS Claim 12; Fig 3; 254bp; English.

XX The invention relates to an isolated secreted/transmembrane PRO
XX polypeptide. The polypeptide and its nucleic acid is useful as an
XX inhibitor of vascular endothelial growth factor stimulated proliferation
XX of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
XX an inducer of endothelial cell apoptosis, c-fos and differentiation of
XX pancreatic beta cell precursors into mature cell, for induction of
XX redifferentiation and/or proliferation of chondrocytes and for modulating
XX glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
XX polypeptide and its nucleic acid is useful for generating transgenic or
XX knock-out animals, for tissue typing and for chromosome identification.
XX The polypeptide is useful in a number of functional biological assays, as
XX molecular weight marker for protein electrophoresis, and as therapeutic
XX agents. The nucleic acid is useful as a hybridisation probe, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX and for the preparation PRO polypeptides. The nucleic acid is also useful
XX as hybridisation probe for a cDNA library to isolate the full length PRO
XX cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
XX useful in the construction of hybridisation probes for mapping the gene
XX encoding PRO, and for the genetic analysis of individuals with the
XX genetic disorders. The present sequence represents the amino acid
XX sequence of a human secreted/transmembrane PRO polypeptide.

SO Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;

Best Local Similarity 100.0%; Pred. No. 2e-63; Mismatches 0; Indels 0; Gaps 0;

DB 1 MIVFGNAVFLASRSICQGLITLLEHIAFLGTGAAITMNSCICRDSGTDSDVDTQ 60
1 MIVFGNAVFLASRSICQGLITLLEHIAFLGTGAAITMNSCICRDSGTDSDVDTQ 60
QY 61 QOAENSAPVTADTRSGPRDPVPPRRGRGPHPRKKQNVQGLVDTLAVIRTLVYDK 117
61 QOAENSAPVTADTRSGPRDPVPPRRGRGPHPRKKQNVQGLVDTLAVIRTLVYDK 117

RESULT 9
ABO44436
ID ABO44436 standard; protein; 117 AA.

AC ABO44436;

DT 01-OCT-2003 (first entry)

DE Human secreted/transmembrane protein PRO444.

XX Human; secreted protein; transmembrane protein; PRO; vulnary; cardiac;
XX antidiabetic; anorectic; antiarthritis; angiogenesis; cancer;
XX adrenal cortical capillary; endothelial; cell growth; wound healing;
XX stimulated T-lymphocyte proliferation; immune response suppression;
XX neonatal heart hypertrophy; cardiac insufficiency disorder;
XX vascular endothelial growth factor; inflammation; mononuclear cell;
XX eosinophil; diabetes; obesity; or hyper-insulinemia; hypo-insulinemia;
XX chondrocyte redifferentiation; bone disorder; cartilage disorder;
XX sports injury; arthritis.

OS Homo sapiens.

EN US2003044841-A1.

XX 06-MAR-2003.

XX 06-DEC-2001; 2001US-00006856.

XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 02-SEP-1998; 98US-0098536P.
XX 02-SEP-1998; 98US-0098596P.
XX 02-SEP-1998; 98US-0098982P.
XX 02-SEP-1998; 98US-0098602P.
XX 02-SEP-1998; 98US-0098642P.
XX 02-SEP-1998; 98US-0098741P.
XX 02-SEP-1998; 98US-0098754P.
XX 02-SEP-1998; 98US-0098763P.
XX 02-SEP-1998; 98US-0098792P.
XX 02-SEP-1998; 98US-0098808P.
XX 02-SEP-1998; 98US-0098812P.
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XX 02-SEP-1998; 98US-0100930P.
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XX 02-SEP-1998; 98US-0101477P.
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XX 02-SEP-1998; 98US-0101916P.
XX 02-SEP-1998; 98US-0102207P.
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XX 02-SEP-1998; 98US-0102330P.
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XX 02-SEP-1998; 98US-0103314P.

PR 07-OCT-1998; 98US-0103315P.
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 PR 22-OCT-1998; 98US-0105199P.
 PR 22-OCT-1998; 98US-0105266P.
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 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
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 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
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 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 28-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
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 PR 10-NOV-1998; 98US-0106934P.
 PR 17-NOV-1998; 98US-0107783P.
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 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
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 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0112296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015284.
 PR 23-AUG-2000; 2000WO-US023352.
 PR 24-AUG-2000; 2000WO-US023358.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US032678.
 PR 01-DEC-2000; 2000WO-US030873.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DU, Ferrara N, Fong S,
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
 PI Williams PW, Wood WI;
 XX
 XX WPI; 2003-492259/46.
 DR N-PSDB; ACH04344.
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating various cardiac insufficiency
 PT disorders, bone and/or cartilage disorders such as sports injuries and
 PT athletes.
 Query Match 100.0%; Score 609; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYFGAVFLASRSIGGGLTLLEHIAHFLTGGAATMGNSICRPDSDGTFDSDVDTQQ 60
 DB 1 MYFGAVFLASRSIGGGLTLLEHIAHFLTGGAATMGNSICRPDSDGTFDSDVDTQQ 60
 QY 61 QQAENSAVPTADTRSGPRDPVPPRRGRGPHHPRRKKQNVGGLVDTTAVIRTLVDK 117
 DB 61 QQAENSAVPTADTRSGPRDPVPPRRGRGPHHPRRKKQNVGGLVDTTAVIRTLVDK 117
 RESULT 10
 ABO33460 standard; protein; 117 AA.
 XX
 AC ABO33460;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
 KW class typing; chromosome identification; vaccine.
 OS Homo sapiens.
 XX
 PN US2003073129-A1.
 XX
 PD 17-Apr-2003.
 XX
 PF 04-SEP-2001; 2001US-00946374.
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 PR 01-SEP-1998; 98US-0098716P.
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PR 20-OCT-1998; 98US-0104987P.
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 PR 26-OCT-1998; 98US-0105633P.
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 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-00218517.
 PR 22-DEC-1998; 98US-0114223P.
 PR 30-DEC-1998; 99MO-US000106.
 PR 05-JAN-1999; 98US-00284291.
 PR 12-APR-1999; 98US-0128674P.
 PR 16-APR-1999; 98US-0144758P.
 PR 23-JUN-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021194.
 PR 18-OCT-1999; 98US-00403287.
 PR 30-NOV-1999; 99MO-US028313.
 PR 02-DEC-1999; 99MO-US028351.
 PR 16-DEC-1999; 99MO-US030095.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 23-AUG-2000; 2000MO-US023522.

24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030352.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 01-JUN-2001; 2001MO-US072035.
PR 01-JUN-2001; 2001MO-US017800.
PR 14-JUN-2001; 2001MO-US082636.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
XX
XX (GETH) GENENTECH INC.
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX WPI: 2003-5585292/55.
DR N-PSDB; ACD67888.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
PS Claim 12; Fig 4; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I), having at least 80% sequence identity to a sequence
Query March 100.0%; Score 609; DB 7; Length 117;
Best local similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIVEGMAVFLASRSLGGGLLTLEEHIAHFLGTGGAATTGNSCTICRDSGTDSDVTQQ 60
1 MIVEGMAVFLASRSLGGGLLTLEEHIAHFLGTGGAATTGNSCTICRDSGTDSDVTQQ 60
DB 1 MIVEGMAVFLASRSLGGGLLTLEEHIAHFLGTGGAATTGNSCTICRDSGTDSDVTQQ 60
QY 61 QQAENSAVPTADTSQPRDPYRPPRRGRGPRRRKKQNVGLVDTLAVIRTLVDK 117
61 QQAENSAVPTADTSQPRDPYRPPRRGRGPRRRKKQNVGLVDTLAVIRTLVDK 117
DB 61 QQAENSAVPTADTSQPRDPYRPPRRGRGPRRRKKQNVGLVDTLAVIRTLVDK 117
RESULT 11
AB019838
ID AB019838 standard; protein; 117 AA.
XX
XX AB019838;
AC
XX
XX 29-AUG-2003 (first entry)
DT
XX
XX Human secreted/transmembrane protein PRO444.
DE
XX
XX Human; PRO; secreted and transmembrane protein; gene therapy;
KM enterocolitis; gastrointestinal ulceration; skin disease; asthma;
KM abdominal keratinocyte differentiation; psoriasis; epithelial cancer;
KM squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KM amyotrophic lateral sclerosis; inflammatory disease; organ failure;
KM rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
KM cardiac injury; birth defect; premature aging; AIDS; cancer;
KM diabetic complication; wound repair.
XX
XX Homo sapiens.
OS
XX
XX US2003044902-A1.
PN
XX
XX 06-MAR-2003.
PD
XX
XX 01-FEB-2002; 2002US-00066193.
PF
XX
XX 26-AUG-1997; 97US-0056974P.

17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062852P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069649P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 10-AUG-1998; 98US-0095988P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 14-SEP-1998; 98MO-US019033.
PR 16-SEP-1998; 98MO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98MO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98MO-US024855.
PR 25-NOV-1998; 98MO-US025190.
PR 01-DEC-1998; 98MO-US025108.
PR 08-MAR-1999; 99MO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99MO-US021252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99MO-US020111.
PR 08-SEP-1999; 99MO-US020594.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021547.
PR 30-NOV-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028565.
PR 07-DEC-1999; 99US-0163495P.
PR 20-DEC-1999; 99MO-US030999.
PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 09-MAR-2000; 2000MO-US006471.
PR 30-MAR-2000; 2000MO-US007377.
PR 30-MAR-2000; 2000MO-US008439.
PR 15-MAY-2000; 2000MO-US013358.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 11-AUG-2000; 2000MO-US020203.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 15-NOV-2001; 2001US-00002796.


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PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102865P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105633P.
PR 26-OCT-1998; 98US-0105642P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105811P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107773P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108856P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113266P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 20-JUL-1999; 98US-0144788P.
PR 26-JUL-1999; 98US-0145698P.
PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 98US-0162506P.
PR 30-NOV-1999; 99WO-US028113.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030873.
PR 10-NOV-2000; 2000WO-US032678.
PR 01-DEC-2000; 2000WO-US036520.
PR 28-FEB-2001; 2001WO-US006652.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX (GENTH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S,
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
XX Williams PM, Wood WI,
XX WPI, 2003-555602/52.
XX N-PSDB; ADIC17874.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 12; SEQ ID NO 6; 555pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The sequences are useful in the preparation of a
XX medicament for treating a condition responsive to a PRO polypeptide. The
XX polypeptides are useful in a number of functional biological assays, as
XX molecular weight markers for protein electrophoresis and as therapeutic
XX
XX Query Match 100.0%; Score 609; DB 7; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2e-63;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGMAVFLASRSIGQGLLTLEHIAHFIQTGAATTMNSCICRDSGTSVDTQQ 60
DB 1 MIVFGMAVFLASRSIGQGLLTLEHIAHFIQTGAATTMNSCICRDSGTSVDTQQ 60
QY 61 QOAEANSVPTADTRQOPRDPVPRPPRGSGPHEPRKKKQNVGLVDTLAVIRTLVKK 117
DB 61 QOAEANSVPTADTRQOPRDPVPRPPRGSGPHEPRKKKQNVGLVDTLAVIRTLVKK 117

RESULT 13
ADDI0295
ID ADDI0295 standard; protein; 117 AA.
XX
XX ADDI0295;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE Human secreted/transmembrane PRO polypeptide #3.

```

XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KM cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KM endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX US2003105011-A1.
 XX
 XX PD 05-JUN-2003.
 XX
 XX PF 16-AUG-2002; 2002US-00223084.
 XX
 XX PR 15-SEP-2000; 2000US-0232887P.
 XX PR 20-JUN-2001; 2001WO-US019692.
 XX PR 09-JUL-2001; 2001WO-US021735.
 XX PR 20-FEB-2002; 2002US-00081056.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillen KJ, Marsters SA, Pan J, Stephan JF,
 PI Watanabe CK, Williams PM, Wood WI, Ye W,
 XX WPI; 2003-810831/76.
 DR N-PSDB; ADD10294.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 PS Claim 11; SEQ ID NO 6; 493bp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 XX SQ Sequence 117 AA;
 XX
 XX Query Match 100.0%; Score 609; DB 7; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2e-63;
 XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQQ 60
 XX DB 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQQ 60
 XX
 XX QY 61 QQAENSNAVPTADTRSGPRDPVPRPRGRGPHPRKKQNDGLVLTAVIRTLVDK 117
 XX DB 61 QQAENSNAVPTADTRSGPRDPVPRPRGRGPHPRKKQNDGLVLTAVIRTLVDK 117
 XX
 XX RESULT 14
 XX ADD11255
 XX ID ADD11255 standard; protein; 117 AA.
 XX AC ADD11255;
 XX

DT 01-JAN-2004 (first entry)
 XX
 XX DE Human secreted/transmembrane PRO polypeptide #3.
 XX
 XX KW human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KM cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KM endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX US2003105013-A1.
 XX
 XX PD 05-JUN-2003.
 XX
 XX PF 16-AUG-2002; 2002US-00223090.
 XX
 XX PR 20-JUN-2001; 2001WO-US019692.
 XX PR 09-JUL-2001; 2001WO-US021735.
 XX PR 20-FEB-2002; 2002US-00081056.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillen KJ, Marsters SA, Pan J, Stephan JF,
 PI Watanabe CK, Williams PM, Wood WI, Ye W,
 XX WPI; 2003-801242/75.
 DR N-PSDB; ADD11254.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide useful for treating a cardiovascular, endothelial, or
 PT angiogenic disorder in a mammal, such as cancer or age-related macular
 PT degeneration.
 XX
 PS Claim 11; SEQ ID NO 6; 493bp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 XX SQ Sequence 117 AA;
 XX
 XX Query Match 100.0%; Score 609; DB 7; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2e-63;
 XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQQ 60
 XX DB 1 MIVFGNAVFLASRLSGGLLTLEHIAHFLGTGAATMGNSCICRDSGTDSDVDTQQ 60
 XX
 XX QY 61 QQAENSNAVPTADTRSGPRDPVPRPRGRGPHPRKKQNDGLVLTAVIRTLVDK 117
 XX DB 61 QQAENSNAVPTADTRSGPRDPVPRPRGRGPHPRKKQNDGLVLTAVIRTLVDK 117
 XX
 XX RESULT 15
 XX ADD70521
 XX ID ADD70521 standard; protein; 117 AA.

XX AC ADD70521;
XX 15-JAN-2004 (first entry)
XX Human secreted/transmembrane protein PRO444.
XX Human; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schönlein-Henoch purpura; Coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX Homo sapiens.
XX US2003099625-A1.
XX 29-MAY-2003.
XX 12-DEC-2001; 2001US-00015386.
XX 01-SEP-1998; 98US-0098776P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
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XX 09-SEP-1998; 98US-0099589P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 13-SEP-1998; 98US-0100385P.
XX 13-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
XX 16-SEP-1998; 98US-0100662P.
XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
XX 17-SEP-1998; 98US-0100684P.
XX 17-SEP-1998; 98US-0100710P.
XX 17-SEP-1998; 98US-0100711P.
XX 17-SEP-1998; 98US-0100919P.
XX 17-SEP-1998; 98US-0100930P.
XX 18-SEP-1998; 98US-0100849P.
XX 18-SEP-1998; 98US-0101014P.
XX 18-SEP-1998; 98US-0101068P.
XX 18-SEP-1998; 98US-0101071P.
XX 22-SEP-1998; 98US-0101279P.
XX 23-SEP-1998; 98US-0101471P.
XX 23-SEP-1998; 98US-0101472P.
XX 23-SEP-1998; 98US-0101474P.
XX 23-SEP-1998; 98US-0101475P.
XX 23-SEP-1998; 98US-0101476P.
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PR 10-NOV-1998; 98US-0107753P.
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PR 18-NOV-1998; 98US-0108851P.
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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.

PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US013705.
 PR 17-MAY-2000; 2000WO-US013705.
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 PR 30-MAY-2000; 2000WO-US015264.
 PR 02-JUN-2000; 2000WO-US023522.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023528.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030973.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
 PI Williams PM, Wood WI;

XX WPI, 2003-974602/81.
 DR N-PSDB; ADD70520.

XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
 PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
 XX Claim 12; SEQ ID NO 6; 553pp; English.

XX The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 609; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: April 2, 2004, 09:52:51
 Job time : 57 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004; 06:40:17 ; Search time 504 Seconds
(without alignments)
9038.793 Million cell updates/second

Title: US-10-066-500-8

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Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	1218	100.0	1218	10	US-10-081-056-5	Sequence 5, Appl
3	1218	100.0	1218	13	US-10-066-500-8	Sequence 8, Appl
4	1218	100.0	1218	13	US-10-002-796-8	Sequence 8, Appl
5	1218	100.0	1218	14	US-10-066-627-8	Sequence 8, Appl
6	1218	100.0	1218	14	US-10-066-494-8	Sequence 8, Appl
7	1218	100.0	1218	14	US-10-066-268-8	Sequence 8, Appl
8	1218	100.0	1218	14	US-10-006-465A-5	Sequence 8, Appl
9	1218	100.0	1218	14	US-10-066-211-8	Sequence 8, Appl
10	1218	100.0	1218	14	US-10-066-193-8	Sequence 8, Appl
11	1218	100.0	1218	14	US-10-006-818A-5	Sequence 8, Appl
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ALIGNMENTS

RESULT 1
US-09-946-374-5
Sequence 5, Application US/03946374
Publication No. US20030072129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Demoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/058716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/058723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/058749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/058750

PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-081-056-5
Sequence 5, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scott A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilian
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02

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US-10-066-500-8
Sequence 8, Application US/10066500
Publication No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Geisler
APPLICANT: Mary E. Gerltisen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavian
APPLICANT: Jennie P. Maher
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
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PRIOR FILING DATE: 1998-02-09
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PRIOR FILING DATE: 1998-03-25
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PRIOR FILING DATE: 1999-03-09
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PRIOR APPLICATION NUMBER: 09/284663
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 09/332928
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/332929

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PRIOR	FILING DATE	1998-09-17	PRIOR	APPLICATION NUMBER	09/248555
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PRIOR	FILING DATE	1998-12-01	PRIOR	APPLICATION NUMBER	09/251900
PRIOR	FILING DATE	1998-11-25	PRIOR	APPLICATION NUMBER	09/050288
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PRIOR	FILING DATE	1999-06-02	PRIOR	APPLICATION NUMBER	09/201111
PRIOR	FILING DATE	1999-09-01	PRIOR	APPLICATION NUMBER	09/205944
PRIOR	FILING DATE	1999-09-08	PRIOR	APPLICATION NUMBER	09/210930
PRIOR	FILING DATE	1999-09-15	PRIOR	APPLICATION NUMBER	09/215474

Query Match	100.0%;	Score 1218;	DB 13;	Length 1218;
Best Local Similarity	100.0%;	Pred. No. 0;		

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Db	61	AAGAGTCGCGCGCGCGCGCGCGCCCTCTCCGATGGGCCCGGAGGTAGAAAGT				120
QY	121	CAGTGCACACGCCGACCCGCGCTGTGAGCCCTGGGACCGCGGAAACGGAGGGAGTCT				180
Db	121	CAGTGCACACGCCGACCCGCGCTGTGAGCCCTGGGACCGCGGAAACGGAGGGAGTCT				180
QY	181	GAGGTTGGGAGCGTCTGTAGGAGGAGGAGAACAGCGCTTGAGCTTGGGCTGGCGAGC				240
Db	181	GAGGTTGGGAGCGTCTGTAGGAGGAGGAGAACAGCGCTTGAGCTTGGGCTGGCGAGC				240
QY	241	GGAAGTGGGCGCGGGGTATGCTCTGGAAAGGGGCCCGGAGAGAGTGTGCTTGGCACAAC				300
Db	241	GGAAGTGGGCGCGGGGTATGCTCTGGAAAGGGGCCCGGAGAGAGTGTGCTTGGCACAAC				300
QY	301	CTGAGAAACAGCCGAGAGGTTTTCCACCGAGCCCGCGCTTGAGGAGTCTGAAAGGTTTC				360
Db	301	CTGAGAAACAGCCGAGAGGTTTTCCACCGAGCCCGCGCTTGAGGAGTCTGAAAGGTTTC				360
QY	361	CTAAGAAAGGTTGTTCCCTCTTTCGGGGGTCCTCACAGAAAGAGGTCTTGAGGGGTGGC				420
Db	361	CTAAGAAAGGTTGTTCCCTCTTTCGGGGGTCCTCACAGAAAGAGGTCTTGAGGGGTGGC				420
QY	421	CTTCTGAGAGGCTGCGGCTTAACAGGGCCCAAGATGSCCATTTGATGTCCAGAAATCCCT				480
Db	421	CTTCTGAGAGGCTGCGGCTTAACAGGGCCCAAGATGSCCATTTGATGTCCAGAAATCCCT				480
QY	481	GTAATTAATATGTTGGGAATTAACCTGTGCACTTCTTTGGCAATTCAGTGTGTAATAAC				540
Db	481	GTAATTAATATGTTGGGAATTAACCTGTGCACTTCTTTGGCAATTCAGTGTGTAATAAC				540
QY	541	AAATGAGATGCMAATTCCTCAACTCCAGTTATGAAACAGACTTGTGGAAACCTGMAAAC				600
Db	541	AAATGAGATGCMAATTCCTCAACTCCAGTTATGAAACAGACTTGTGGAAACCTGMAAAC				600
QY	601	TACCTAATATATGCTCTTTGGTTGGGCGGATTTTACGAGACAGAAAGCTTGGCCAGGG				660
Db	601	TACCTAATATATGCTCTTTGGTTGGGCGGATTTTACGAGACAGAAAGCTTGGCCAGGG				660
QY	661	TCTGTGTGTGACTCTCGAAGAGCATATAGCCCATCTTCTGAGGACTGAGGTTGCCGTAC				720
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QY	721	TACAGATGGGTATTCGTGTATCTGATCTGCCAGATGACAGTGGAAACAGATGACATGTGTACAC				780
Db	721	TACAGATGGGTATTCGTGTATCTGATCTGCCAGATGACAGTGGAAACAGATGACATGTGTACAC				780
QY	781	CCAAACAGCAAGSCCGAGAACAGTGCATGCCATCTGTGACACACAAAGAACCAACACG				840
Db	781	CCAAACAGCAAGSCCGAGAACAGTGCATGCCATCTGTGACACACAAAGAACCAACACG				840
QY	841	GGAACCTTTCGGCGCAACCAAGAGGGGCGAGGACCTCATAGACCAAGAGAAAGAAACA				900
Db	841	GGAACCTTTCGGCGCAACCAAGAGGGGCGAGGACCTCATAGACCAAGAGAAAGAAACA				900
QY	901	AAATGTGATGGGCTAGTGTGGACACACTGGCAGTAAATAGGACTCTGTGATGATAGTA				960
Db	901	AAATGTGATGGGCTAGTGTGGACACACTGGCAGTAAATAGGACTCTGTGATGATAGTA				960
QY	961	AGTATCTGACTCAGCGTCACTCCAGTGGAAATGAAAATGTTCTTCCCGGAAACCATGACT				1020
Db	961	AGTATCTGACTCAGCGTCACTCCAGTGGAAATGAAAATGTTCTTCCCGGAAACCATGACT				1020
QY	1021	TTAGAGCTCTTCAAGTTCCTTTTGAACATCTCCGCAAGCCTTGTGTCTCACAGGGCAAG				1080
Db	1021	TTAGAGCTCTTCAAGTTCCTTTTGAACATCTCCGCAAGCCTTGTGTCTCACAGGGCAAG				1080

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Page 7

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DB 1081 GAGATATTTTAAATGCTCCGTCAGTAAATGATTTGTTTCTT 1140
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DB 1141 GCGTCTACTCTTTTGTCTGGAATGCTTAAATGTTTCTGTCAGAAAACGATTAAG 1200
QY 1201 CTATGATCTTTATTAGG 1218
DB 1201 CTATGATCTTTATTAGG 1218

RESULT 4

US-10-002-796-8
Sequence 8, Application US/10002796
Publication No: US20030032057A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltisen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas P. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Wickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE REFERENCE: P3130R1C1
CURRENT FILING DATE: 2001-11-15 796
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16

PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
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 QY 1201 CTATGATCTTTATTAGAG 1218
 Db 1201 CTATGATCTTTATTAGAG 1218
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 US-10-066-273-8
 ; Sequence 8, Application US/10066273
 ; Publication No. US2003002062A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi
 ; APPLICANT: Kevin P. Baker
 ; APPLICANT: David A. Botstein
 ; APPLICANT: Luc Desnoyers
 ; APPLICANT: Dan L. Eaton
 ; APPLICANT: Napoleone Ferrara
 ; APPLICANT: Sherman Fong
 ; APPLICANT: Wei-Qiang Gao
 ; APPLICANT: Hanspeter Gerber
 ; APPLICANT: Mary E. Gerritsen
 ; APPLICANT: Audrey Goddard
 ; APPLICANT: Paul J. Godowski
 ; APPLICANT: Austin L. Gurney
 ; APPLICANT: Ivar J. Kjaevlin
 ; APPLICANT: Jennie P. Macher
 ; APPLICANT: Mary A. Napier
 ; APPLICANT: James Pan
 ; APPLICANT: Nicholas F. Paoni
 ; APPLICANT: Margaret Ann Roy
 ; APPLICANT: Timothy A. Stewart
 ; APPLICANT: Daniel Tumas
 ; APPLICANT: Colin K. Watanabe
 ; APPLICANT: P. Mickey Williams
 ; APPLICANT: William I. Wood
 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3130R1C2
 ; CURRENT APPLICATION NUMBER: US/10/066,273
 ; CURRENT FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: 10/002,796
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
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 ;; PRIOR FILING DATE: 1999-03-05
 ;; PRIOR APPLICATION NUMBER: 09/284663
 ;; PRIOR FILING DATE: 1999-04-15
 ;; PRIOR APPLICATION NUMBER: 09/332928
 ;; PRIOR FILING DATE: 1999-06-14
 ;; PRIOR APPLICATION NUMBER: 09/332929

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Db 1141 GCTGTCATCTACTTTGCTGCTGGAATGCTTAAATGTTTCTGTCGACAGAAACCGATPAAG 1200
QY 1201 CTATGATCTTTATTAGAG 1218
Db 1201 CTATGATCTTTATTAGAG 1218

RESULT 6
US-10-066-494-8
Sequence 8, Application US/10066494
Publication No. US2003002063A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaevn
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tunas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130P1C
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
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PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25

PRIOR APPLICATION NUMBER: 60/066994
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
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PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 09/284663
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PRIOR APPLICATION NUMBER: 09/332928
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PRIOR APPLICATION NUMBER: 09/332929


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62 PRIOR APPLICATION NUMBER: PCT/US99/12252
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64 PRIOR APPLICATION NUMBER: PCT/US99/20111
65 PRIOR FILING DATE: 1999-09-01
66 PRIOR APPLICATION NUMBER: PCT/US99/20594
67 PRIOR FILING DATE: 1999-09-08
68 PRIOR APPLICATION NUMBER: PCT/US99/21090
69 PRIOR FILING DATE: 1999-09-15
70 PRIOR APPLICATION NUMBER: PCT/US99/21547

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Query Match	100.0%;	Score 1218;	DB 14;	Length 1218;
Best Local Similarity	100.0%;	Pred. No. 0;		

[illegible]

Mon Apr 5 09:54:03 2004

us-10-066-500-8.rnpb

Page 13

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Db 1141 GCTGTCACTACTTGTGCTGAAATGCTAAATGTTCTGTACAGAAAACGATTAAG 1200
QY 1201 CTATGATCTTTATTAAGAG 1218
Db 1201 CTATGATCTTTATTAAGAG 1218

RESULT 7
US-10-066-269-8
Sequence 8, Application US/10066269
Publication No. US2003040014A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Geisler
APPLICANT: Mary E. Gerlitsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaevan
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C4
CURRENT APPLICATION NUMBER: US/10/066,269
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
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 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 09/US99/21547

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DB	121	CAGTGCACAGCCCGACCGCGCTGCTGTAGAGCTTGGGACCGGAAACGGAAGTCT	180		
QY	181	GAGGTTGGGACGCTGTGAGAGGAGGAGACGCGCTGCGCGCGCGCGCGCGCG	240		
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QY	241	GACTGGGCGCGGAGTGTCTGTGAAAGGCGCGCGGAGAGTGTGCGTGTGAGAC	300		
DB	241	GACTGGGCGCGGAGTGTCTGTGAAAGGCGCGCGGAGAGTGTGCGTGTGAGAC	300		
QY	301	CTGAGAAACAGCCGAGAGGTTTCCACCGAGCGCGCTTGAAGGATCTGAAGGTT	360		
DB	301	CTGAGAAACAGCCGAGAGGTTTCCACCGAGCGCGCTTGAAGGATCTGAAGGTT	360		
QY	361	CTGAGAAAGGAGTGTCTCTTCTGCGGAGTCTTCCACCAAGAGGTTCTTGGGAGT	420		
DB	361	CTGAGAAAGGAGTGTCTCTTCTGCGGAGTCTTCCACCAAGAGGTTCTTGGGAGT	420		
QY	421	CTTCTGAGAGGCTGCGCTTACAGGCGCCAGAACTTGCATGTGAGATGCAATCCCT	480		
DB	421	CTTCTGAGAGGCTGCGCTTACAGGCGCCAGAACTTGCATGTGAGATGCAATCCCT	480		
QY	481	GTAAGTGTATATGTGAGAAATAGCTCTGCAATCTTCTTGGATCACTGTGTAAGAA	540		
DB	481	GTAAGTGTATATGTGAGAAATAGCTCTGCAATCTTCTTGGATCACTGTGTAAGAA	540		
QY	541	AAATAGATGCAATTTCTTCACTCCAGGTTATGAAACAGTATCTTGAAGAACTGAAG	600		
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DB 1201 CTATGATCTTTATTAAG 1218

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; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 5
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-856A-5

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAGGAGTGCAGCG 120
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DB 121 CAGTCCCAACAGCCG 180
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QY 361 CTAGAGAGGAGTGTTCCTCTTTTCGGGGGTCTTCACCAAGAGGTTCTTGGGGGTGCC 420
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DB 841 GGACCCCTGTGGCGCACACAGAGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
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RESULT 9
US-10-066-211-8
; Sequence 8, Application US/1006211
; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara

APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
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APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaevlin
APPLICANT: Jennie P. Matner
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C8
CURRENT APPLICATION NUMBER: US/10/066,211
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
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PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922

PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/109304
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PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1999-06-15
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PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/149396
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 08/918874
PRIOR FILING DATE: 1997-08-26
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PRIOR FILING DATE: 1999-08-25
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PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/423844
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18

APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mathier
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C3
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18


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APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C4
CURRENT APPLICATION NUMBER: US/10/006,818A
CURRENT FILING DATE: 2001-12-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO: 5
LENGTH: 1218
TYPE: DNA
ORGANISM: Homo sapiens
US-10-006-818A-5

Query Match
Best Local Similarity 100.0%; Score 1218; DB 14; Length 1218;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCGCGCGCGCTGCGCTGCACTCTTGTCTCTGGAAGTGTGCA 60
DB 1 CCCACGCGTCCGCGCGCGCGCTGCGCTGCACTCTTGTCTCTGGAAGTGTGCA 60
QY 61 AAGGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 AAGGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 CAGTGCACAGCCCGACCGCGCGCTGCTGAGCCCTGAGGACGCGGAGCGGAGTCT 180
DB 121 CAGTGCACAGCCCGACCGCGCGCTGCTGAGCCCTGAGGACGCGGAGCGGAGTCT 180
QY 181 GAGGCTGGGAGAGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GAGGCTGGGAGAGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 GAGGCTGGGAGAGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 GAGGCTGGGAGAGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 CTGAGAAACAGCCGAGAGGTTTCCACCGAGGCGCGCGCTTGAAGAGGTTTC 360
DB 301 CTGAGAAACAGCCGAGAGGTTTCCACCGAGGCGCGCGCTTGAAGAGGTTTC 360
QY 361 CTGAGAGAGGAGGTTTCCCTCTTTCGAGGAGGTTTCCACCGAGAGGTTTTCGCG 420
DB 361 CTGAGAGAGGAGGTTTCCCTCTTTCGAGGAGGTTTCCACCGAGAGGTTTTCGCG 420
QY 421 CTCTGAGAGGAGGTTTCCCTCTTTCGAGGAGGTTTCCACCGAGAGGTTTTCGCG 480
DB 421 CTCTGAGAGGAGGTTTCCCTCTTTCGAGGAGGTTTCCACCGAGAGGTTTTCGCG 480
QY 481 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 AATAGAGATGCAATCTCTCACTCCAGGTTATGAAAACAGTATCTTGAAGAACTGAAAC 600
DB 541 AATAGAGATGCAATCTCTCACTCCAGGTTATGAAAACAGTATCTTGAAGAACTGAAAC 600
QY 601 TACTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 TACTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 TCTGTGTGTGATCTCTGAGAGAGCAATAGCCCACTTCTAGGAGCTGAGGAGTGCCTAC 720
DB 661 TCTGTGTGTGATCTCTGAGAGAGCAATAGCCCACTTCTAGGAGCTGAGGAGTGCCTAC 720
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QY 721 TACATGAGTAAATTCCTGATCTGCGAGATGACAGTGGAAACAGATGACAGTGTGAC 780
DB 721 TACATGAGTAAATTCCTGATCTGCGAGATGACAGTGGAAACAGATGACAGTGTGAC 780
QY 781 CCAACAGCAACAGGCGGAGAAACAGTGCAGTACCCTGCTGACAAAGAGGCAACAG 840
DB 781 CCAACAGCAACAGGCGGAGAAACAGTGCAGTACCCTGCTGACAAAGAGGCAACAG 840
QY 841 GAGCCTGTTGCGCCACCAAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GAGCCTGTTGCGCCACCAAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 AATGTGATGAGGCTGATGTTGAGACACTGCGAGTATAGGACTCTTGTGATGATG 960
DB 901 AATGTGATGAGGCTGATGTTGAGACACTGCGAGTATAGGACTCTTGTGATGATG 960
QY 961 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 TTAGAGCTCCTTCACTGCTTTAGAGCACTGCGCAAGCTTGTGCTCAAGGCAAG 1080
DB 1021 TTAGAGCTCCTTCACTGCTTTAGAGCACTGCGCAAGCTTGTGCTCAAGGCAAG 1080
QY 1081 GAGAAATTTTAAATGCTCGCTGATGAGAGTAAATGATGATGATGATGATGATG 1140
DB 1081 GAGAAATTTTAAATGCTCGCTGATGAGAGTAAATGATGATGATGATGATGATG 1140
QY 1141 GCTGTCACTACTTGTGTGAAATGCTTAAATGTTTGTGACAGAAACAGATTAAG 1200
DB 1141 GCTGTCACTACTTGTGTGAAATGCTTAAATGTTTGTGACAGAAACAGATTAAG 1200
QY 1201 CTATGATCTTATTAAG 1218
DB 1201 CTATGATCTTATTAAG 1218
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RESULT 12

US-10-015-393A-5
Sequence 5, Application US/10015393A
Publication No. US2003069179A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C4
CURRENT APPLICATION NUMBER: US/10/015,393A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO: 5
LENGTH: 1218
TYPE: DNA
ORGANISM: Homo sapiens
US-10-015-393A-5

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCCAAGCGCTCCGAGCGCGGTGGCCCTGGGTGCACATCTTTGGCGGTTCTCTCGGACCTGTGCACA	60
Db	1	CCCAAGCGCTCCGAGCGCGGTGGCCCTGGGTGCACATCTTTGGCGGTTCTCTCGGACCTGTGCACA	60
QY	61	AAGAGTCCGCGCGCGCGCGCGCCCTCCCTCCGTGGGCGCGGAGGTAGAGAAGT	120
Db	61	AAGAGTCCGCGCGCGCGCGCGCCCTCCCTCCGTGGGCGCGGAGGTAGAGAAGT	120
QY	121	CAGTGCACACAGCCCGACCGGCTGTGTAGACCTTGGGACACGGGAACTGGGAGGGAGTCT	180
Db	121	CAGTGCACACAGCCCGACCGGCTGTGTAGACCTTGGGACACGGGAACTGGGAGGGAGTCT	180
QY	181	GAGGGTTGGGAGCCTCTGTGAGGAGGAGGAAACAGCCCTCGAGCTTGGGCGCGGACCC	240
Db	181	GAGGGTTGGGAGCCTCTGTGAGGAGGAGGAAACAGCCCTCGAGCTTGGGCGCGGACCC	240
QY	241	GGACTGGGCGCGGGGTGAGCTCTGGAAAAGGCCCGGAGAGAGGTGGCTTGGTCAAAAC	300
Db	241	GGACTGGGCGCGGGGTGAGCTCTGGAAAAGGCCCGGAGAGAGGTGGCTTGGTCAAAAC	300
QY	301	CTGAGAAACAGCCGAGAGGTTTCCACCGAAGGCCCGGCTTGAGAGGATCTGAAGAGTTTC	360
Db	301	CTGAGAAACAGCCGAGAGGTTTCCACCGAAGGCCCGGCTTGAGAGGATCTGAAGAGTTTC	360
QY	361	CTAGAAGAGGTTGTTCCCTCTTTGGGGGTCTTCAACAAGAGGTTCTTTGGGGTGGCC	420
Db	361	CTAGAAGAGGTTGTTCCCTCTTTGGGGGTCTTCAACAAGAGGTTCTTTGGGGTGGCC	420
QY	421	CTTCTGAGAGAGCTGCGGCTTACACAGGGCCCAAGCTGCATTGGATGTCCAGATCCCTCT	480
Db	421	CTTCTGAGAGAGCTGCGGCTTACACAGGGCCCAAGCTGCATTGGATGTCCAGATCCCTCT	480
QY	481	GTAGTTGATATGTTGGGAATAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAC	540
Db	481	GTAGTTGATATGTTGGGAATAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAC	540
QY	541	AAATAGGATGCAAAATTCCTCAATTCGAGGTTATGAAAACAGTACTTGGAAAACGAAAC	600
Db	541	AAATAGGATGCAAAATTCCTCAATTCGAGGTTATGAAAACAGTACTTGGAAAACGAAAC	600
QY	601	TACCTAAATGATCGCTTTGTTGGGCGGTGTTCTTAGCGAAGAACCTTGGCCAGGG	660
Db	601	TACCTAAATGATCGCTTTGTTGGGCGGTGTTCTTAGCGAAGAACCTTGGCCAGGG	660
QY	661	TCTGTTGTGACTCTCGAAGACATAGGCCCATTTCTTAGGAGCTGGAAGTGGCCGCTAC	720
Db	661	TCTGTTGTGACTCTCGAAGACATAGGCCCATTTCTTAGGAGCTGGAAGTGGCCGCTAC	720
QY	721	TACCATGGGTATATCTGTATCTGCGAGATGACAGTGGAAACAATGACAGTGTGACAC	780
Db	721	TACCATGGGTATATCTGTATCTGCGAGATGACAGTGGAAACAATGACAGTGTGACAC	780
QY	781	CCAAACAGCAAGGCGGAGAACAGTGCAGTACCCACTGCTGACACAGAGGCCAACACAG	840
Db	781	CCAAACAGCAAGGCGGAGAACAGTGCAGTACCCACTGCTGACACAGAGGCCAACACAG	840
QY	841	GGAACCTTGGGAGCCACCAAGAGAGGGGCGGAGACCTCATAGCCAGAGAAAGAAACA	900
Db	841	GGAACCTTGGGAGCCACCAAGAGAGGGGCGGAGACCTCATAGCCAGAGAAAGAAACA	900
QY	901	AAATGTGATGGGCTAGTGTGACACACTGGCACTAATACGGACTTGTGTAGTAAGTA	960
Db	901	AAATGTGATGGGCTAGTGTGACACACTGGCACTAATACGGACTTGTGTAGTAAGTA	960
QY	961	AGTATCTGATCAAGGTACCTCCACGTGGATGAAAAGTGTTCGCGGAGAACATGACT	1020
Db	961	AGTATCTGATCAAGGTACCTCCACGTGGATGAAAAGTGTTCGCGGAGAACATGACT	1020
QY	1021	TTAGGACTCTTCAGTTCTTTAGACATACCTGCGCAAGCCTTGTGTCAACAGGCAAG	1080
Db	1021	TTAGGACTCTTCAGTTCTTTAGACATACCTGCGCAAGCCTTGTGTCAACAGGCAAG	1080
QY	1081	GAGAAATTTTATGCTCCGCTGATGGCAGAGTAAATGATTAAGATTGATGTTTTGCTT	1140

[illegible]

Db 721 TACCATGGGTAACTCTGATCTGCCAGATGACGTGAAACAGATGACATGTTGACAC 780
Qy 781 CCACAGCAACAGCCGAGACAGTGCAGTACCCACTGCTGACACAGAGCAACACCG 840
Db 781 CCACAGCAACAGCCGAGACAGTGCAGTACCCACTGCTGACACAGAGCAACACCG 840
Qy 841 GGAACCTGTTGGCCACACAGAGAGGGGGCCGAGACCTTCACTGAGCCACAGAGAAAGAAAC 900
Db 841 GGAACCTGTTGGCCACACAGAGAGGGGGCCGAGACCTTCACTGAGCCACAGAGAAAGAAAC 900
Qy 901 AAATGTGATGGAGTGTGTGACACACTGCAGTAATACGACCTTGTAGATAAGTA 960
Db 901 AAATGTGATGGAGTGTGTGACACACTGCAGTAATACGACCTTGTAGATAAGTA 960
Qy 961 AGTATCTGACTCAGCGTCACTCCAGTCCAGTCACTGCTGCTCACAGGGCAAG 1020
Db 961 AGTATCTGACTCAGCGTCACTCCAGTCCAGTCACTGCTGCTCACAGGGCAAG 1020
Qy 1021 TTAGGACTCCTCTAGTCTCTTGAAGACATCTCGCCAGCCTTGTGCTCACAGGGCAAG 1080
Db 1021 TTAGGACTCCTCTAGTCTCTTGAAGACATCTCGCCAGCCTTGTGCTCACAGGGCAAG 1080
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Db 1081 GAGAAATTTTAAATGCTCCGCTGATGCAAGTAATGATTAAGATTGATGTTTGTCTT 1140
Qy 1141 GCTGTCACTACTTGTCTGTGAAATGCTAAATGTTCTGTAGAGAAAACAGATTAAG 1200
Db 1141 GCTGTCACTACTTGTCTGTGAAATGCTAAATGTTCTGTAGAGAAAACAGATTAAG 1200
Qy 1201 CTATGATCTTTATTAGAG 1218
Db 1201 CTATGATCTTTATTAGAG 1218

RESULT 15
US-10-006-116A-5

Sequence 5, Application US/10006116A
Publication No. US20030082626A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Destroyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C15
CURRENT APPLICATION NUMBER: US/10/006,116A
PRIOR FILING DATE: 2001-12-16
PRIOR APPLICATION NUMBER: 60/098716
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475


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Db      721 TACCATGGTAAATTCCTGTATCTGCCGAGATGACAGTGAACAGATGACAGTGTGACAC 780
QY      781 CCAACAGCAACAGGCCCGAAGAACAGTGAATACCACTGCTGACACAGAGAGCCCAACACG 840
Db      781 CCAACAGCAACAGGCCCGAAGAACAGTGAATACCACTGCTGACACAGAGAGCCCAACACG 840
QY      841 GGAACCTGTTGCGGCCACCAAGAGAGGCGCAGAGACCTCATGAGCCCAAGAGAAAGAACCA 900
Db      841 GGAACCTGTTGCGGCCACCAAGAGAGGCGCAGAGACCTCATGAGCCCAAGAGAAAGAACCA 900
QY      901 AAATGTGATGGGCTAGTGTGACACACTGGCAATATACGACTCTTGTAGATTAAGTA 960
Db      901 AAATGTGATGGGCTAGTGTGACACACTGGCAATATACGACTCTTGTAGATTAAGTA 960
QY      961 AGTATCTGACTCAGCGGTCACTCCAGTGAATGAAAGTGTCTGCGCCGGAACCATGACT 1020
Db      961 AGTATCTGACTCAGCGGTCACTCCAGTGAATGAAAGTGTCTGCGCCGGAACCATGACT 1020
QY      1021 TTAGGACTCCTTCAAGTTCCTTTAGGACATACTGCCCAAGCCTTGTGCTCACAGGSCAAAG 1080
Db      1021 TTAGGACTCCTTCAAGTTCCTTTAGGACATACTGCCCAAGCCTTGTGCTCACAGGSCAAAG 1080
QY      1081 GAGAAATTTTAAATGCTCCGCTGATGSCAGATPAATGATTAAGATTGATGTTTGGCTT 1140
Db      1081 GAGAAATTTTAAATGCTCCGCTGATGSCAGATPAATGATTAAGATTGATGTTTGGCTT 1140
QY      1141 GCTGTCATCTACTTTGTCTGAAAAATGCTAAATGTTTCTGTAGCAGAAAAACAGATPAAG 1200
Db      1141 GCTGTCATCTACTTTGTCTGAAAAATGCTAAATGTTTCTGTAGCAGAAAAACAGATPAAG 1200
QY      1201 CTATGATCTTTATTAGAG 1218
Db      1201 CTATGATCTTTATTAGAG 1218

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Search completed: Apr:1 4, 2004, 09:11:21
 Job time : 512 secs

Dy 465 ATGTCAGAAATCCCTGTAGTTGATAATGTTGGGAATAAGCTCTG 509
| | | | |
Db 1066 ATCGCAAGCTCCCTGCACCTGCAGCCAAGCTCGGAATTATTCTG 1022

RESULT 4
US-08-789-329C-1

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1  GENERAL INFORMATION:      ET AL.
2  APPLICANT:  SHERWOOD
3  TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
4  TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
5  NUMBER OF SEQUENCES:  20
6

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Query Match 3.5%; Score 42.2; DB 3; Length 6529;

QY	4	ACGGCTCCGGGGCGCGCTGGCGCTGGCGCTCCATCTTTCCGCTTCTCTCGAAGCTCTCAACAAG	63
Db	5433	AGGCGCGCGCACCCGGGGCTCGGGCTCCCTCCCGCGGGCAAGCCCGGGGTGTGCATCG	5492
QY	64	GAGTGGCGCGCGCGCGCGCGCCCTCCCTCCGATGGGCCCGCGGAGTAGAGAAAGTCAG	123
Db	5493	GAGCGAACCCCTCCCGGGAGCGATGCATATATGATGGGGGGGGGGGGAGAGCGTCT	5552
QY	124	TGCCACAGCCGACCCGCGCTGCTCTTGAGGCTTGGGCATGCGGAAACGGAGGAGTCTGAG	183
Db	5553	CGCTCCGCGCGCGCCCGCCCTTTGCTTGCCCGGAGAAATCGCGGGCGCGGGGCGGGATTAG	5612
QY	184	GCTTGGGGACGCTGTGAGGGAGGGGGAACAGCCGCTCGAGCCTGGGGCGGG	234
Db	5613	GCGCCGGGGTGTGGGCTTGGGGTTAGGGCCCGGGATTGGATCGGGCCCGG	5663

RESULT 5
US-08-615-170-20/c
; Sequence 20, Application US/08615170
; Patent No. 576776
GENERAL INFORMATION:

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Query Match 3.48; Score 41.2; DB 1; Length 1894

QY 11 CGGCGCGCGGCGCGCGCATCTTTCCGCTTCTCGAACCTGTACAAAGAGTCGC 70

Db 475 CTGCTCAATATCCGGGCTCCACACTCCCTCGGCGCTATTGTCCAGGCTCTTCCATCCC 416

QY 71 GCGCGCGCGCGCGCGCCCTCCCTCCGATGGGCGCGGAGGTAGAAATGTCAGTCCACA 130

Db 415 GTCTCGGCAATCTTCCGCGCCCTCCCGGGGTGTGCTGGCGTTCCAGCTTTGGACGC 356

QY 131 GCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGACGGAAGGAGTCTAGGGTTGG 190

Db 355 TATGTGCTGCTGCTGCTGTGGCTCTGAAACCCGAGCCCCACGACACGAACTGCT 296

QY 131 GACGCTCTGAGGAGGAGGGAACAGCGCGCTCGAGCTGTGGGCGGCGC--GACCGGACTGG 248

Db 295 CCGTACTCCGAGGCGCTGACCGCAACGAGGAGCGGAGATGATGATCCGGGACCGAAACGG 236

QY 249 GCCGGGCTAGGCTCTGGAAGGCGCCGGAGAGAG 283
DB 235 ACCGGAGCCGGTGCCTGGGATGATGATCCGGGGAGAG 201

RESULT 6

US-08-615-170-18/c
Sequence 18, Application US/08615170
Patent No. 5776776

GENERAL INFORMATION:
APPLICANT: ORDAHL, Charles P.
APPLICANT: AZARIE, Anthony
APPLICANT: MAR, Janet H.
APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah E.
APPLICANT: STEWART, Alexander F.R.
APPLICANT: LARKIN, Sarah B.
TITLE OF INVENTION: DTER-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-615-170-18

Query Match 3.4%; Score 41.2; DB 1; Length 1897;
Best Local Similarity 48.4%; Pred. No. 0.077;
Matches 133; Conservative 3; Mismatches 137; Indels 2; Gaps 1;

QY 11 CGCGCGCGTGGCTCGCTTCATCTTTGCGCTTCTCTCGAGCTCTCAAAAGAGTCGC 70
DB 475 CTGCTCAATGTCGGGCTCCACATCCCTCGCGTTCATGTCACAGCTCTTGTCCATCCC 416
QY 71 GCGCGCGCGCGCGCGCGCTCCCTCGCGGTGGCGCCGGGAGGTAGAAAGTAGTGGCCACA 130
DB 415 GTCTGTGCGCATTTCCCGCCCTCCCGGAGGCTGCTGCTGAGGCTTCCAGCTTTGAGAGC 356
QY 131 GCCCGACCGCGCTGCTCTGAGCCCTGGGACGCGGAAACGGAGGAGGTCTGAGGGTTGGG 190

DB 355 TATGTGCTGCTGCTCTGCTGCTGCTGAGCCCGAGCCCCACGACACAGAACTGCT 296
QY 191 GAGCTCTGTAGAGGAGAGGAGAAACCGCTCGAGCTGAGGCGGGC--GGACCGAATGGG 248
DB 295 CCGTGTCTCCGAGAGGCTGAGCCGKCCACCGGAGCCCGGAGTGTGCCGAGACCGAGC 236
QY 249 GCCGGGCTAGGCTCTGGAAGGCGCCGGAGAGAG 283
DB 235 ACCGGAGCCGCTGCCGGGATGATGATCCGGGGAGAGG 201

RESULT 7

US-09-060-756-4
Sequence 4, Application US/09060756
Patent No. 6183957

GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1280
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-060-756-4

Query Match 3.3%; Score 40.8; DB 3; Length 1280;
Best Local Similarity 47.0%; Pred. No. 0.081;
Matches 126; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 38 GCGCTCTCTCGAGCTGTGCAAAAGATGCGCGCGCGCGCCCGCTCCCTCCG 97
DB 523 GCGGCTAGCCGACGAGGCTGCTGCTGCGCAGCGCGCGCGCGCGCGCGGATTTGGT 582
QY 98 TGGGCGCGGAGGTAGAGAAAGTCACTGTCACACGCCGACCGGCTCTGTAGCCCTGG 157
DB 583 TTCTCTCGTGGGACCGCGCGCGCGCGCGCGCTGTCTGTGTCACGCGCGG 642
QY 158 GCAAGCGGAGCGGAGGAGTCTGAGGCTTGGGAGCATCTGTGAGGAGGAGAACGCG 217
DB 643 GCGGCGGCTTCCGCGGCTTCCGACCGCGGCTGCGGCGCGCGCGCGCGCATATGCC 702
QY 218 CTGAGCTTGGGCG 277
DB 703 GCGTGGCTGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 762
QY 278 AGAGAGTGGCGCTTGTGCAAGACCTGAG 305
DB 763 GCGCGCGGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 790

RESULT 8
US-09-670-314-4
Sequence 4, Application US/09670314
Patent No. 6492506

GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
FILE REFERENCE: 3495-0169

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1 CURRENT APPLICATION NUMBER: US/09/670,314
2
3 CURRENT FILING DATE: 2001-01-12
4
5 PRIOR APPLICATION NUMBER: 09/060,756
6
7 PRIOR FILING DATE: 1998-04-16
8
9 NUMBER OF SEQ ID NOS: 743
10
11 SOFTWARE: Patentin Ver. 2.0
12
13
14 SEQ ID NO. 4
15
16 LENGTH: 1280
17
18 TYPE: DNA
19
20 ORGANISM: Mycobacterium tuberculosis
21
22 US-09-670-314-4

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Query Match      3.3%; Score 40.8; DB 4; Length 1280;
Best Local Similarity 47.0%; Pred. No. 0.081;
Matches 126; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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Qy	38	GCGGTTCTCGAGAACCTGTACAAAAGATGCGCGCGCGCGCGCCCTCCCTCGG	97
Db	523	GGCGGTAGCCACAGGCTCTCTGTTTCGACAGCGCGCGCGCGCGCGATTGGT	582
Qy	98	TGGGCCCCGGAGTAAAGAAAGTCAAGTGCACAGCCGACCGCGTCTCTGAGCCCTGG	157
Db	583	TTCTCTCGTGGGAGCGCGCGGCGCGGTGGCAAGCCGGGCTGCTGTTGTTCAGCGGCGG	642
Qy	158	GCAAGCGGAAACGGAGAGGAGTCTGAAGGTTGGAGGAGCTGTGAGAGGAGGGGAAACACCG	217
Db	643	GCCGCGCGGTTCCGCGGCTTCGGCACCCGCGGTGGGTGCGTGGAGCGCGGCGCAATGCC	702
Qy	218	CTCGAGCTTGAGGCGGAGCCGACCGGACTGAGGCGGAGTGAAGCTCTGAGAAAGGCCCGG	277
Db	703	GGCTGCTTGGCTTCGCGCGGAGCCGGGAGCATCGCGGAATCGCGGTAACGTAAACGG	762
Qy	278	AGAGAGGTGCGCTTGTGTCAAACTGAG	305
Db	763	GGCGCGGTGAGAACCGGCGCACCGCGG	790

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RESULT 9
US-09-165-264-11
; Sequence 11: Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vainayagamorthy, Thuraiyah
; TITLE OF INVENTION: Multi-Loei Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ. ID NOS.: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

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[illegible]

RESULT 10
US-09-866-108A-15742/C

```

/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: FENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OR INVENTION: MYOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOINCA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecmica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 15742
/ LENGTH: 500
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-15742

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Query Match	3.2%	Score 39.4	DB 4	Length 500	
Best Local Similarity	48.3%	Pred. No. 0.12			
Matches 103; Conservative	0	Mismatches 106	Indels 0	Gaps 0	

[illegible]

RESULT 11
US-09-754-250-3
; Sequence 3, Application US/097542506
; Patent No. 6376225
; GENERAL INFORMATION:

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/ APPLICANT: WEI, Ming-Hui et al
/ TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
/ TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
/ FILE REFERENCE: C1001063
/ CURRENT APPLICATION NUMBER: US/09/754,250
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 111282
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(111282)
/ OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3
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```
Query Match
Best Local Similarity 50.5%; Score 39.2; DB 4; Length 111282;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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QY 102 CCGGAGGTAGTGAAGTCAAGTCCACAGCCCGGAGCTGCTGAGCCCTGAGCAGC 161
DB 39453 CCGAGGCGAGACAGAAAGCGGGTGAACGCGCGGCTGCTCGGTGAGGATCGG 39512
QY 162 GCGGAAAGGAGGAGCTGAGGAGTGGGAGCTCTGTGAGGAGGAGGAGGAGGAG 221
DB 39513 ACAGGCGGAGAGGAGTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39572
QY 222 AGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281
DB 39573 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39632
QY 282 AGGTGGCG 289
DB 39633 CTGTGCGG 39640
```

```
RESULT 12
US-09-252-991A-5281/C
/ Sequence 5281, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 5281
/ LENGTH: 723
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5281
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```
Query Match
Best Local Similarity 47.1%; Score 39; DB 4; Length 723;
Matches 120; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
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```
QY 8 GTCCGGGCGGCGCTCGGCTCATCTTGCCTCTCTCGGACCTGCACAAAGAGT 67
DB 571 GCCCCAGGCGCGCCGCGCGCGCGCGGAGATGTCGCGACCGCCCTCCGGGAGC 512
QY 68 CCGCGCCGCGCGCGCGCGCGCGCTCTCTCGGTGGCGCGGAGGTAGAGAAAGTGC 127
DB 511 GATGGCCAGCGCGGCGCGCGCGCGCTCTCCAGAGGTAGATGATGCTCGAACCC 452
```

```
QY 128 ACAGCCGACCGCGCTGCTGAGCCCTGGGACAGCGGAAAGGAGGAGTCTGAGGCT 187
DB 451 CTGGCCATAGGAGAGCGGCTCCGCGCGGAGCCCTGCTGCGGCGGAGCGGCGGAGC 392
QY 188 GGGAGCTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
DB 391 CTGGGCTCGGAGGCGGATATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 332
QY 248 GGGCGGGTATGAGCTC 262
DB 331 GCGCAGGCGGCTTC 317
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RESULT 13
US-09-252-991A-5345/C
/ Sequence 5345, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 5345
/ LENGTH: 744
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5345
```

```
Query Match
Best Local Similarity 47.1%; Score 39; DB 4; Length 744;
Matches 120; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
```

```
QY 8 GTCCGGGCGGCGCTCGGCTCATCTTGCCTCTCTCGGACCTGCACAAAGAGT 67
DB 602 GCCCGAGGCGCGCGCGCGCGCGCGCGCGGAGATCTCGGACCGCCCTCCGGGAGC 543
QY 68 CCGCGCGCGCGCGCGCGCGCGCTCTCTCGGTGGCGCGGAGGTAGAGAAAGTGC 127
DB 542 GATGGCCAGCGCGGCGCGCGCGCGCGCTCTCCAGAGGTAGATGATGCTCGAACCC 483
QY 128 ACAGCCGACCGCGCTGCTGAGCCCTGGGACAGCGGAAAGGAGGAGTCTGAGGCT 187
DB 482 CTGGCCATAGGAGAGCGGCTCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
QY 188 GGGAGCTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
DB 422 CTGGGCTCGGAGGCGGATATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
QY 248 GGGCGGGTATGAGCTC 262
DB 362 GCGCAGGCGGCTTC 348
```

```
RESULT 14
US-09-252-991A-5307/C
/ Sequence 5307, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
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Search completed: April 4, 2004, 09:02:45
Job time: 131 secs

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5307
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5307

Query Match      3.2%; Score 39; DB 4; Length 954;
Best Local Similarity 47.1%; Pred.No. 0.23;
Matches 120; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 8 GTCCGCGCCCGCTGGCTCGCTCCATCTTTGCGGCTTCTTCGACCTGTCAACAAGAGT 67
DB 849 GCCCAGGAGCGCGCGCGCGCGCGCGCGCGCGAGATGTCGCGACGACGCGCTCCGAGGC 790
QY 68 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127
DB 789 GATGCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 730
QY 128 ACAGCCCGACCGCGCTGCTTGAGCCTTGCGCACGCGGACGCGAGAGTCTGAGGCTT 187
DB 729 CTGGCCATAGCGCGACGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 670
QY 188 GGGGACGTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 247
DB 669 CTGGAGGTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 610
QY 248 GGGCGGGGTAGGCTC 262
DB 609 GGCCAGGCGCGGTTC 595

RESULT 15
US-09-292-034-1
; Sequence 1, Application US/09292034
; Patent No. 6492343
; GENERAL INFORMATION:
; APPLICANT: Reddy, P. Seshidhar
; APPLICANT: Tikoo, Suresh
; APPLICANT: Babliix, Lorne
; TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
; FILE REFERENCE: 293102002400
; CURRENT APPLICATION NUMBER: US/09/292,034
; CURRENT FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 34094
; TYPE: DNA
; ORGANISM: Porcine Adenovirus Type 3
; FEATURE:
US-09-292-034-1

Query Match      3.2%; Score 38.4; DB 4; Length 34094;
Best Local Similarity 54.2%; Pred.No. 2.4;
Matches 78; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 34 CTTTGCCGTTCTCTGCACTGTCAACAAGAGTGCAGCGCGCGCGCGCGCGCGCGCGCT 93
DB 31399 CTCTGCGGAGCAACCACTCCCGCTCGTGAATGCTTCTTCTCCCGCGCGCTGCGCC 31458
QY 94 CCGGTGGCGCGCGGAGTAGAAGTAGTAGTGCACAGCCGACCGCGGCTGAGCC 153
DB 31459 CCGATGGCTTCGCGCGCGCGCTTCAAGCCAGCGCGCAAGCGCTGGCGCGCGCGAGCC 31518
QY 154 CTGGGACGCGGAGACGAGGAG 177
DB 31519 ACCGGCTGCTTCACTGTCGAG 31542
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 05:01:37 ; Search time 3064 Seconds

(without alignments)
11870.802 Million cell updates/sec

Title: US-10-066-500-8
Perfect score: 1218
Sequence: 1 cccacgcgtccgcgcgcgtg.....agctatgattcttatagag 1218

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_eebba:*
2: em_eebba:*
3: em_eebba:*
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29: em_eebba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	727	59.7	801	12	BG772050 602721686
2	688	56.5	781	14	CD109369 AGENCOURT
3	686.8	56.4	701	14	CA295705 12B22056
4	683.2	56.1	760	13	BG576035 UT-H-E21-

Result No.	Score	Query Match	Length DB	ID	Description
5	602.8	49.5	3391	11	AK032416
6	582.8	47.8	591	14	CB2955706
7	550.4	45.2	892	12	BG152534
8	535.4	44.0	722	12	BG744401
9	505.4	41.5	711	12	B1666950
10	505.4	41.5	835	13	B161287
11	505.4	41.5	857	13	BUS00574
12	505.4	41.5	871	13	BQ439291
13	503.8	41.4	670	12	CG683922
14	503.8	41.4	727	12	BG749354
15	503.8	41.4	834	12	B1668768
16	499.4	41.0	588	11	B0072529
17	498	40.9	1821	11	AK043522
18	493.4	40.5	692	12	BG699229
19	483.2	39.7	700	9	AU253442
20	482.8	39.6	611	14	CD690089
21	478.6	39.3	899	10	BP937383
22	478.2	39.3	742	10	BB82864
23	477.8	39.2	908	14	CA978792
24	477.6	39.2	623	13	BA482659
25	464.6	38.1	789	12	BG620045
26	456.8	37.5	921	12	BM010902
27	440.4	36.2	556	12	BG773383
28	436.8	35.9	862	14	CB183456
29	434.4	35.7	579	14	CD691874
30	430.8	35.4	560	9	AL703545
31	428.4	35.2	531	12	BG719220
32	421.6	34.6	893	13	BQ899613
33	405.6	33.3	745	12	B1768690
34	397.8	32.7	518	14	CA392843
35	388.2	31.9	936	10	BP781079
36	387.2	31.8	1939	11	AK076799
37	384.8	31.6	629	13	BY729431
38	382	31.4	510	29	CG542955
39	380.2	31.2	420	13	BK487789
40	380	31.2	394	10	AN296811
41	376.4	30.9	405	9	AA373599
42	366	30.0	819	9	AU080966
43	365.6	30.0	475	13	BX529453
44	360.2	29.6	488	29	CG608250
45	352	28.9	723	12	BG165215

ALIGNMENTS

RESULT 1
LOCUS BG772050
DEFINITION 602721686F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838565 5', mRNA sequence.
ACCESSION BG772050
VERSION BG772050.1 GI:14082703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiyaki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLM10772 row: 1 column: 22


```

OY 297 GAACCTGAGAAACAGCCGAGAGGTTTTCACCAAGCCCGGCTTGAGGATCGAAGAG 356
Db 265 GAACCTGAGAAACAGCCGAGAGGTTTTCACCAAGCCCGGCTTGAGGATCGAAGAG 324
OY 357 GTTCTTAGAAGAGGAGTGTTCCTTTTCGGGGGCTTCACCAAGAGGTTCTTGGGGGT 416
Db 325 GTTCTTAGAAGAGGAGTGTTCCTTTTCGGGGGCTTCACCAAGAGGTTCTTGGGGGT 384
OY 417 CGCCCTTGTGAGGAGGCTGAGGCTAACAGAGGCGCAAGACTGCAATGATGTCAGATC 476
Db 385 CGCCCTTGTGAGGAGGCTGAGGCTAACAGAGGCGCAAGACTGCAATGATGTCAGATC 444
OY 477 CCCTGTAGTATATATGTTGGAAATAGCTCTGCAACTTCTTGGCAATTCAGTTTAA 536
Db 445 CCCTGTAGTATATATGTTGGAAATAGCTCTGCAACTTCTTGGCAATTCAGTTTAA 504
OY 537 AAACAAATAGATGTAATTCCTCAATCCAGGTTTAAACAGTCTTGGAAATGTA 596
Db 505 AAACAAATAGATGTAATTCCTCAATCCAGGTTTAAACAGTCTTGGAAATGTA 564
OY 597 AAACCTAATATATGCTCTTGTGGGCGGCTTCTTAGCAGAGAGAGCCCTGGCC 656
Db 565 AAACCTAATATATGCTCTTGTGGGCGGCTTCTTAGCAGAGAGAGCCCTGGCC 624
OY 657 AGGCTCTGTTGTAAGTCTCGAAGAGCATAGCCCACTTCTTAGGAGCTGAGAGT-CC 715
Db 625 AGGCTCTGTTGTAAGTCTCGAAGAGCATAGCCCACTTCTTAGGAGCTGAGAGT-CC 684
OY 716 GCTACTACCAT-GGGTAATTCCTGATCTG-CCGAGATGACAGTGAACAGATGACAGT 773
Db 685 GCTACTACCATGAGGTAATTCCTGATCTG-CCGAGATGACAGTGAACAGATGACAGT 744
OY 774 -TTGACACCCCAACAGCAACAGGCC 796
Db 745 TTGACACCCCAACAGCAACAGGCC 768

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RESULT 3
CB295705 701 bp mRNA linear EST 28-FEB-2003
LOCUS 12822056 rev_1_E02_r_007.ab1 Chimpanzee brain library Koo's Pan
troglodytes cDNA clone 12822056_rev_1_E02_r_007.ab1 5', mRNA
DEFINITION
CB295705.1 GI:28621135
ACCESSION
CB295705.1 GI:28621135
KEYWORDS
EST.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
1 (bases 1 to 701)
Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and
Paabo, S.
Selection on human genes as revealed by comparisons to chimpanzee
cDNA
JOURNAL
Genome Res. (2003) In press
COMMENT
Contact: Paabo S
Evolutionary Genetics
Max-Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Tel: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
Email: paabo@eva.mpg.de
Seq primer: M3 reverse.
FEATURES
source
location/Qualifiers
1..701
/organism="Pan troglodytes"
/mol_type="mRNA"
/db_xref="taxon:9598"
/clone="12822056_rev_1_E02_r_007.ab1"
/sex="male"
/tissue_type="brain, presumably cortex"
/dev_stage="adult"

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/lab host="Epilcurian Coli (TM) XL-10-Gold"
/clone lib="Chimpanzee brain library Koo's"
/notes=Vector: pUC1; Site 1: SfiI-A; Site 2: SfiI-B; The
library was prepared using the SMART cDNA library
construction kit (Clontech), doing only primer extension,
but not PCR amplification of the cDNA. The only deviation
from the published protocol was that we cloned the cDNA
into a plasmid vector."

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ORIGIN

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Query Match 56.4%; Score 686.8; DB 14; Length 701;
Best Local Similarity 98.7%; Pred. No. 4,1e-164;
Matches 688; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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OY 261 TCTGAAAGAGGCGCGGAGAGAGTGGCGTTGATCGAAGCTGAGAAACAGCCGAGAGT 320
Db 1 TCTGAAAGAGGCGCGGAGAGAGTGGCGTTGATCGAAGCTGAGAAACAGCCGAGAGT 60
OY 321 TTTCACCCGAGGCGCGCTTAGAGGATCTGAAAGAGTTCCTAGAAAGAGGAGTCCCTC 380
Db 61 TTTCACCCGAGGCGCGCTTAGAGGATCTGAAAGAGTTCCTAGAAAGAGGAGTCCCTC 120
OY 381 TTTCGAGGAGTCTCAACAGAGAGTCTTGGAGGCTGCGCTTCTAGAGAGGCTGCGCT 440
Db 121 TTTCGAGGAGTCTCAACAGAGAGTCTTGGAGGCTGCGCTTCTAGAGAGGCTGCGCT 180
OY 441 AACAGGCGCCAGAACTGCCATTGATGCCAATCCCTGATGTTGATATGTTGGAA 500
Db 181 AACAGGCGCCAGAACTGCCATTGATGCCAATCCCTGATGTTGATATGTTGGAA 240
OY 501 TAAGCTGCAACTTCTTGGCATTCAGTGTGTAACCAATAGATGACAAATTCCTC 560
Db 241 TAAGCTGCAACTTCTTGGCATTCAGTGTGTAACCAATAGATGACAAATTCCTC 300
OY 561 AACTCCAGTTATGAAACAGTACTTGAAACCTGAAACCTAATGATGCTCTTG 620
Db 301 AACTCCAGTTATGAAACAGTACTTGAAACCTGAAACCTAATGATGCTCTTG 360
OY 621 GTTGGCGGTTCTTAGAGAGAGAGGCTGGCGAGGCTGTTGATGACCTGGAAG 680
Db 361 GTTGGCGGTTCTTAGAGAGAGAGGCTGGCGAGGCTGTTGATGACCTGGAAG 420
OY 681 AGCAGATAGCCCACTTCTTAGAGAGAGGCTGGCGAGGCTGTTGATGACCTGGA 740
Db 421 AGCAGATAGCCCACTTCTTAGAGAGAGGCTGGCGAGGCTGTTGATGACCTGGA 480
OY 741 TCTCCGAGATGACAGTGAACAGATGACAGTGTGACACCCCAACAGCAACAGCCGAGA 800
Db 481 TCTCCGAGATGACAGTGAACAGATGACAGTGTGACACCCCAACAGCAACAGCCGAGA 540
OY 801 ACAGTCAGTACCCACTGCTGACACAGAGAGCCCAACAGGAGCCTGTTGGCCACCA 860
Db 541 ACAGTCAGTACCCACTGCTGACACAGAGAGCCCAACAGGAGCCTGTTGGCCACCA 600
OY 861 GAGAGGCGCGAGAGACTCTAGAGCCAGAGAGAAACAAATGTGATGGCTAGTGT 920
Db 601 GAGAGGCGCGAGAGACTCTAGAGCCAGAGAGAAACAAATGTGATGGCTAGTGT 660
OY 921 TGAGACACTGGAGTATACGAGTCTTGTGATTA 957
Db 661 TGAGACACTGGAGTATACGAGTCTTGTGATTA 697

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RESULT 4
B0576035/c 760 bp mRNA linear EST 19-JUN-2002
LOCUS B0576035
DEFINITION
UT-H-EZ1-bbg-c-03-0-UI-51 NCI CGAP chr2 Homo sapiens cDNA clone
UT-H-EZ1-bbg-c-03-0-UI 3', mRNA sequence.
ACCESSION
B0576035
VERSION
B0576035.1 GI:21479352
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

```


REFERENCE
1 (bases 1 to 760)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
Seq primer: M13 FORWARD
PolyA=yes

FEATURES
source

Location/Qualifiers
1..760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ1-dbg-c-03-0-UI"
/tissue_type="chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lemon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 56.1%; Score 683.2; DB 13; Length 760;
Best Local Similarity 98.9%; Pred. No. 3,5e-163;
Matches 696; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
515 TTCTTGGCATTAGTGTAAACAAATAGATGCAATTCCTCACTCCAGGTTATG 574
721 TTCTTGGCATTAGTGTAAACAAATAGATGCAATTCCTCACTCCAGGTTATG 663
575 AAAACAGTACTTGAAGAACTGAAGAACTACCTAATATGATGCTTTGGCCCTGTTTC 634
662 AAAACAGTACTTGAAGAACTGAAGAACTACCTAATATGATGCTTTGGCCCTGTTTC 603
635 TTTCGAG 694
602 TTTCGAG 543
695 TTTCGAG 754
542 TTTCGAG 483
755 AGTGAAG 814
482 AGTGAAG 423
815 ACTGCTGACACAG 874

Db 422 ACTGCTGACACAG 363
Qy 875 CCTCATGAGCCAG 934
Db 362 CCTCATGAGCCAG 303
Qy 935 GTAATACGAGACTTGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 994
Db 302 GTAATACGAGACTTGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 243
Qy 995 AAGTGTCTGCGCCGAGACCATGATCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTG 1054
Db 242 AAGTGTCTGCGCCGAGACCATGATCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTG 183
Qy 1055 CCAAGCTGTGTCTCAAGGCGAAG 1114
Db 182 CCAAGCTGTGTCTCAAGGCGAAG 123
Qy 1115 AATG 1174
Db 122 AATG 63
Qy 1175 TTCTGTAGACAG 1218
Db 62 TTCTGTAGACAG 19
RESULT 5
AK032416
LOCUS
DEFINITION
MUS musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430540K8 product:hypothetical sp1a and
the Rianodine Receptor (SPRY)/SPRY domain/RING finger containing
protein, full insert sequence.
AK032416
AK032416.1 GI:26328234
HTC; CAP trapper.
MUS musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
TITLE
JOURNAL
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
TITLE
JOURNAL
MEDLINE
20530913
PUBMED
11076861
REFERENCE
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs <i>Nature</i> 420, 563-573 (2002)
TITLE	6 (bases 1 to 3391)
JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harada, A., Hashinuma, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hoti, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kochi, H., Kawai, J., Koizumi, Y., Kondo, S., Komuro, H., Kouda, M., Koya, S., Kuwahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saio, R., Satoh, H., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, Y., Muramatsu, M. and Hayashizaki, Y.
COMMENT	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc@riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.genic.riken.go.jp/ Location/Qualifiers
FEATURES source	1..3391 <code>/organism= "Mus musculus"</code> <code>/mol_type= "mRNA"</code> <code>/strain= "C57BL/6J"</code> <code>/db_xref= "FANTOM DB:6430540K08"</code> <code>/db_xref= "MG1:2395918"</code> <code>/db_xref= "taxon:10090"</code> <code>/clone= "6430540K08"</code> <code>/sex= "male"</code> <code>/tissue_type= "olfactory brain"</code> <code>/clone_id= "RIKEN full-length enriched mouse cDNA library"</code> <code>/dev_stage= "adult"</code> 606_-..2336 <code>/note= "unnamed protein product: hypothetical Spia and the Ryanodine Receptor (SPRY)/SPRY domain/RING finger containing protein (InterPro IPR003877, InterPro IPR003878, InterPro IPR001841, evidence: putative"</code> <code>/codon_start= 1</code> <code>/protein_id= "BAC27658.1"</code> <code>/db_xref= "gi:26328235"</code> <code>/translation= "MTVGMAYFLASRSIQGLLITLBEBIAHLICTGATRMNNGSICRDSGADNDVTQQAENSSTVFTHAASQSDPVPVPRGRGPHPRKKQAVDLYLDIAVIRILVDNDOSPPYSMTLIHMAEDBGMDLVYOSLIVLEPDLGAVALTLIDCEPLPTCDALOKSTEILNTNGEVACDPSGHAPAKRNITSAYLGAEIAGPAVALIGLAPGLEIYLLOCTLOSHPTLPVLLAIEMERKAQSENKLTTSESSIPRLTVAITLMADPDYLRQVGRCQAOMSLDNLFKEGRQLTYEKRDNLNTRAMLNSNDSEYLIKTIPIRGELRADASSFEBSVRCIFCYDTGTGVYYETVYTSGVMQIGMARDRSKFNHBGYGDDSEISCAVDGCRLIWYNARKSPHVHPQWEGDVTGVLIDLNENQM.FLAGNDLPPEKRVSSVTSGFFAAFSMSYQQCSFGGEAFPKYPSNKIRSTENDYVFLTAEEKIIIIIPRRRIALLIKVYSIRENCSSLCCDEAVDTOLFKPCGHSDLCMDCALOETCPCKREIIVSRIRQISHIS"</code>
ORIGIN	Query Match 49.5%; Score 602.8; DB 11; Length 3391; Best Local Similarity 80.3%; Pzed No. 2.1e-142;

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QY	11	CGGCGCGGTGGCCCTCGCGTGCATCTTTGGCGGTCTCTCGGACCTGTACAAAGAGTCGC				70
Db	20	CAGTGCCTGTCCCGCGGTCACTTTTACCGCTCTCTTGGACCTGTACAAAGAGTCGC				79
QY	71	GCGCGCGCGCGCGCCCTCTCCCTCCGGTGGGCCCGGAGGTAGAGAAAGTCAGTCCACA				130
QY	131	GCCCGACCGGCGTCTGTCTGANG-----CCCTGGGACGCGGAAAGGGAGGGAGTCTGAGGG				185
QY	140	GCCCGACCGGCGTCTGTGGAAAGCCCTTTGGGAGCTGTGCGCGGAGGGAGCTTGAGGG				199
QY	186	TTGGGAGCTGTCTGTGAGGAGGGGAAACAGCCGCTCGAGCTGTGGGCGCGGCGGACCTG				245
Db	200	CTAGCGACGCGCTGTGAAGAGAGGGGACAGCGCGCTGAAGCTGTGGGTGCGAGGACGTGACT				259
QY	246	GGGGCGCGGGGTAGGCTTGTGAAAAGGCCCGGAGAGAGGTGGCGTTGTCAAGACCTGAG				305
Db	260	GGGGCGCGGTGCGCGTCTCCGGGCAAGGGGTCTTGAAGAGGGTGGCGTTGTCAAGACCTGAG				319
QY	306	AAACAGCGCGAAGGTTTTCACGAGAGCGCGCGCTTAGGAGATGTGAAGAGTCTCTAGA				365
Db	320	AAGAGCGCGGACACACATCTCTCGAGGCGCGCGCTGAGAGCGCTGAAGCGTCTCTGG				379
QY	366	AGAGGAGTTCCTCTTTGCGGGGCTCTCAACAGAGAGTTCCTTGGGGGTGCGCCCTTCT				425
Db	380	AAGAGGAGTTCCTCTTTGCGGGGCTCTTGAAGAGAGGTCTCT--GGGGTCAACCTCTCC				437
QY	426	GAGAGGCTCGCGGTACAGAGGCCCAACATGCGCATTTGAGATGTCAGAAATGCCCTGAGT				485
Db	438	GAGAGAGC-----CGGCTAAGAACCTGCGAGTGAATGGCCACATTTCCACAGTGT				486
QY	486	TGATAAATGTTGGGATAAGCTGTGCAACTTCTTTGGCATTCAGTTGTTAAAAACAATA				545
Db	487	TGATAAATGTTGGAAATAGCTGTGACCTTCTTCACACATTCAGTTGTTAAAAATGATA				546
QY	546	GGATGCATAATTCCTCAACTCGAGTTTGAATAACGTAATTGGAAAACTGAAAATCTACT				605
Db	547	GAAATGCAGAT---TCAGTTCCACATTTGAATAACAGTACTCGGAAAAATGAAAATCTACT				603
QY	606	AAATGATCGTCTTGGTTGGGGCGGTGTTCTTAGAGGACAGAGGCTTGGCGAGGGTCTGT				665
Db	604	AGATGATTTGCTTTGGTTGGGCTGTGTTCTTTAGACAGAAAGCTTGTGCGGGTGTGC				663
QY	666	TGTTAGCTCTGAGAGACACATAGCCCACTTCTAGGAGCTGAGAGTGGCGGCTACTACCA				725
Db	664	TGCTGACTCTTGAAGACACATAGCCCACTATTTGGGAGCTACAGTGGCCACTCTCTACTA				723
QY	726	TGGGTATTTCTGTGATTTGCCGAGATGACAGTGGAAACAGATGACAGTGTGACACCCAAC				785
Db	724	TGGGTAAATCTCTGTATCTGCCGAGATGACAGTGGAGCAGAAACAAATGTTGACACCCAC				783
QY	786	AGCAACAGCGCGAGACAGTGCAGTACCACTGCTGACACAAAGAGCCAAACAGCGGACC				845
Db	784	AGCAACAGCGCTGAGAACAGTACATAGTCCCTACTGCTGATGAGAGCCAACTCGGAGCC				843
QY	846	CTGTTCCGCCACCAAGAGGGGCCGAGACCTCACTGAGCCAAAGAGAAAGAAACAATATG				905
Db	844	CTGTCGGGCTCTCAAGAGAGGCGGAGAGACTCTATGAGCCCAAGAGAAAGAAACAATATG				903
QY	906	TGATATGGCTATGTGTGACACACTGCGCAGTAAATACGACTCTTGTAGTATA				957
Db	904	TGATATGGGTATGTGTGTGACACACTGCGCGGTAAATACGACTCTTGTAGTATA				955
RESULT 6						
CB295706						
LOCUS						
DEFINITION						
	CB295706	591 bp	mRNA	linear	EST 28-FEB-2003	
	12822056	rev 1	A02_r_005	ab1 Chimpanzee brain library	Xcos Pan	
	troglodytes	CDNA clone 12822056	rev 1	A02_r_005	ab1 5', mRNA	
					sequence.	

ACCESSION	CB925706
VERSION	CB925706.1
KEYWORDS	GI:28621136
SOURCE	EST.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Pan troglodytes
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan. 1 (bases 1 to 591)
TITLE	Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and Paabo, S.
JOURNAL	Selection on human genes as revealed by comparisons to chimpanzee cDNA
COMMENT	Genome Res. (2003) In press Contact: Paabo S Evolutionary Genetics Max-Planck-Institute for evolutionary Anthropology Deutscher Platz 6, 04103 Leipzig, Germany Tel: +49-(0)-341-3550 500 Fax: +49-(0)-341-3550 555 Email: paabo@eva.mpg.de Seq primer: M13 reverse.
FEATURES	Location/Qualifiers
source	1..591
	/organism="Pan troglodytes"
	/mol_type="mRNA"
	/db_xref="taxon:9598"
	/clone="12832056_rev_1_A02_r_005.ab1"
	/sex="male"
	/tissue_type="Brain, presumably cortex"
	/dev_stage="adult"
	/lab_host="Epilaurian Cell (TM) XL-10 Gold"
	/clone_lib="Chimpanzee brain library Koo's"
	/note="Vector: pUC19; Site 1: SfiI-A; Site 2: SfiI-B; The library was prepared using the SMART cDNA library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid vector."
ORIGIN	
Query Match	47.8%; Score 583.8; DB 14; Length 591;
Best Local Similarity	99.3%; Pred. No. 1.4e-137;
Matches	584; Conservative 0; Mismatches 4; Indels 0; Gaps 0
QY	265 GAAAGGGCCCGGAGAGAGAGTGGCGTTGGTCAGAACTGAGAAACAGCCGAGAGGTTTTC 324
Db	4 GGANNGGCCCGGAGAGAGAGTGGCGTTGGTCAGAACTGAGAAACAGCCGAGAGGTTTTC 63
QY	325 CACGAGAGCCCGCGCTTGAGGGATCTGAAGAAGTTCTGAGAGAGGAGTTCCTCTTTC 384
Db	64 CACGAGAGCCCGCGCTTGAGGGATCTGAAGAAGTTCTGAGAGAGGAGTTCCTCTTTC 123
QY	385 GGGGTTCTACAGAAAGGTTCTTGGGGGTGCGCCCTTCTGAGAGAGGCTGCGGCTTACA 444
Db	124 GGGGTTCTACAGAAAGGTTCTTGGGGGTGCGCCCTTCTGAGAGAGGCTGCGGCTTACA 183
QY	445 GGGCCAGACATGCCATTGGATGTCAGAAATCCCGTGAATTGATTAATTTGGAAATAG 504
Db	134 GGGCCAGACATGCCATTGGATGTCAGAAATCCCGTGAATTGATTAATTTGGAAATAG 243
QY	505 CTCTGCAACTTCTTTGGCATTCAAGTTGTTTAAAAACAATATAGATGCAAAATTCCTCACT 564
Db	244 CTCTGCAACTTCTTTGGCATTCAAGTTGTTTAAAAACAATATAGATGCAAAATTCCTCACT 303
QY	565 CCAGGTTAAGAAACAGTACTTGGAATCTGAATTAATCTAATAGATGCTTTGGTGG 624
Db	304 CCAGGTTAAGAAACAGTACTTGGAATCTGAATTAATCTAATAGATGCTTTGGTGG 363
QY	625 GGCCTGTTCTTAGCAGAGAGAAAGCCTTGCCAGAGGCTGTTGTTGACTCTCGAAAGAGA 684
Db	364 GGCCTGTTCTTAGCAGAGAGAAAGCCTTGCCAGAGGCTGTTGTTGACTCTCGAAAGAGA 423
QY	685 CATAGCCCACTTCATAGGAGCTGAGAGTGCCTGCTACTACATAGGGAATATTCCTGATCTG 744

Db	Accession	Source	Score	Length	Gap
Db	424	CATAGCCCACTTCTCTAGGACTGGAGGTGCTGCTACTACATGGGTAATTCCTATCTG	483		
Qy	745	CCGAGATGACAGTGGAAACAATGACATGTGTGACACCAACAGACAAGGCCAGAAACAG	804		
Db	484	CCGAGATGACAGTGGAAACAATGACATGTGTGACACCAACAGACAAGGCCAGAAACAG	543		
Qy	805	TGCAGTACCACTGCTGACACAAGAGCCCAACCAACGAGACCTGTTGCG	852		
Db	544	TGCAGTACCACTGCTGACACAAGAGCCCAACCAACGAGACCTGTTGCG	591		
RESULT 7	BUI52634	892 bp mRNA linear EST 03-SEP-2002			
DEFINITION	AGENCOURT 8750338 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6333149				
ACCESSION	BUI52634				
VERSION	BUI52634.1	GI:22666166			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 892)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgs@bgl-remail.nih.gov Tissue Procurement: Mark Macconochie, Ph.D. and Nancy L. Freeman, Ph.D.				
FEATURES	Source				
FEATURES	Location/Qualifiers				
FEATURES	1..892				
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FEATURES	/clone="IMAGE:6333149"				
FEATURES	/lab_host="DH10B (phage-resistant)"				
FEATURES	/clone_id="NIH_MGC_130"				
FEATURES	/note="Organ: oocytes; Vector: pCMV-SPORT6.1; Site: 1; EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH_MGC library."				
ORIGIN					
Query Match	45.2%; Score 550.4; DB 13; Length 892;				
Best Local Similarity	79.2%; Pred. No. 3.1e-129;				
Matches	711; Conservative 0; Mismatches 166; Indels 21; Gaps 4;				
Qy	40	CGTCTCTCGGACCTGTCACAAAGAGTCGCGCCGCGCCGCGCCCTCCCTCCGCTG	99		
Db	1	CGTCTCTTGGACCTGTACCAAAGAGTCGCGCCGCTCTCGCTCTCCCTCCGCTG	60		
Qy	100	GCGCCGCGAGGTAGAGAAAGTCAGTGCACAGCCCGACCGCGCTGCTTGAAG----	154		
Db	61	GCGCCGAGAGGTAGAGCAAGTCAGTGCACAGCCCGACCGCGCTGCTTGGAAAGCCCT	120		
Qy	155	TGGGACCGCGAAGCGGAGGAGTCTGAGGATTTGGGACGCTCTGAGAGGAGGACAG	214		
Db	121	TGGGACCGCGGAGGAGGAGGAGTCTGAGGAGTCTGAGAGGAGGAGGAGGAG	180		
Qy	215	CGCTCGAGCCTTGGGCGCGGCGAGACCGGACTGGGCGCGGAGTCTGAGAAAGGCTC	274		
Db	181	CGCTCGAGCCTTGGGCGCGGCGAGACTGGGCGCGGAGTCTGAGAAAGGCTC	240		

QY 275 GGGAGAGAGTGTGGCGTTGGTGTGACAGTGAAGAAACAGCCAGAGTTTCCACCGAGGC 334
 DB 241 TTGGAGAGAGTGTGGCGTTGGTGTGACAGTGTGGAAGAACCCGCGACACTCTCTCCGAGGCC 300
 QY 335 CGCGCTTGAAGAGTGTGGAAGAGTGTCTTGAAGAGAGGTGTCTCTCTTGGGGGTCTTC 394
 DB 301 CGCGCTTGAAGAGTGTGGAAGAGTGTCTTGAAGAGAGGTGTCTCTCTTGGGGGTCTTC 360
 QY 395 ACCAGAGAGTGTCTTGGGGGTTCGCCCTTCTGAGAGAGTGGCGCTAACAGGGCCAGAA 454
 DB 361 ACTGAAGAGAGTCTCT--GGGATCACCTCCCGAGAGACT-----GGCTAAGAA 407
 QY 455 CTGCGATTGATGTCTGAGAAATCCCGTGTGATGATTAATGTTGGGAATAGCTTGCACCT 514
 DB 408 CTGCGAGTGTATGGCGAGCATTTCCAGTGTGATTAATGTTGAATAGACTGCTTGAACC 467
 QY 515 TTCTTTGGCATTCATCTTGTAAAAAACAATAGATGCAAAATCTCTCAACTCCAGGTTATG 574
 DB 468 TTCTTCAGCATTCAGTGTGTAAAAATGATGAAATGCAAGT---TCAGTTCCACATTATG 524
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 QY 815 ACTGTGACACAGAGAGCAACACGAGGACCTGTGGGACCAAGAGAGGGCCGAGGA 874
 DB 765 ACTGTGATGATGAGAGCAACCTGAGACCTCTTCCGCTCTCAAGAGAGGCGCAGGA 824
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 DEFINITION 602723139F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849713 5',
 mRNA sequence.
 ACCESSION BG744401
 VERSION BG744401.1 GI:14055054
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Tissue: testis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 722)
 NIH-MGC http://mgi.mgi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rtm1.nih.gov
 Tissue Procurement: Dr. Daniel McGivern, DBS/NCI
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L16C1689 row: m column: 10
 High quality sequence stop: 676.

FEATURES
 source
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4849713"
 /issue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
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 /note="Organ: blood; Vector: pTZ19.1; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 44.0%; Score 535.4; DB 12; Length 722;
 Best Local Similarity 99.5%; Pred. No. 1.9e-125; Indels 2; Gaps 2;
 Matches 558; Conservative 0; Mismatches 1;
 QY 398 AGAAGAGTCTTGGGGGTGCGCTTCTGAGAGAGCTGGGCTAAAGAGGCCAGACTG 457
 DB 2 AGAAGAGTCTTGGGGGTGCGCTTCTGAGAGAGCTGGGCTAAAGAGGCCAGACTG 61
 QY 458 CCAATGAGATGCAAGATCCCTGTATGATTAATGTTGGATTAAGCTTGGCACTTC 517
 DB 62 CCAATGAGATGCAAGATCCCTGTATGATTAATGTTGGATTAAGCTTGGCACTTC 121
 QY 518 TTGGCATTCAGTGTGTAATAACAATAGATGCAAAATCTCTCAACTCCAGTTATGAA 577
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 DB 182 ACGATCTTGGAAAACTGAAATCTAATGATGCTTTGTTGGGCGTGTCTTA 240
 QY 638 GCGAGAGAGAGCTTGGGAGAGGTCTGTTGATGCTCTGAGAGACATAGCCACTTC 697
 DB 241 GCGAGAGAGAGCTTGGGAGAGGTCTGTTGATGCTCTGAGAGACATAGCCACTTC 300
 QY 698 CTAGGACTGAGAGTGGCGCTACTACATGAGTAAATCTCTGATCTGCCAGATGACAT 757
 DB 301 CTAGGACTGAGAGTGGCGCTACTACATGAGTAAATCTCTGATCTGCCAGATGACAT 360
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 DB 361 GGAACAGATGACAGTGTACACCCACAGCAAGAG--CCGAGACAGTGCATGCCAC 420
 QY 817 TGCTGACACAGAGAGCAACAGGACCTGTTGGCCACCAAGAGAGGGCCGAGAAC 876
 DB 421 TGCTGACACAGAGAGCAACAGGACCTGTTGGCCACCAAGAGAGGGCCGAGAAC 480
 QY 877 TCATGAGCCAGAGAGAAACAAATGTGATGGGTAGTGTGACACACTGGCAGT 936
 DB 481 TCATGAGCCAGAGAGAAACAAATGTGATGGGTAGTGTGACACACTGGCAGT 540
 QY 937 AATAGGAGCTCTTGTATGATTA 957
 DB 541 AATAGGAGCTCTTGTATGATTA 561
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 mRNA sequence.
 ACCESSION B1666950
 VERSION B1666950.1 GI:15581183
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

	ORGANISM	Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	REFERENCE	1 (Bases 1 to 711)
	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
	JOURNAL	Unpublished (1999)
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bse-remail.nih.gov Tissue Procurement: Miklos Palokovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizuki Toshiyuki and Piero Carninci (RIKEN) DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LLM11788 row: p column: 02 High quality sequence stop: 695.
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	source	1..711
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		/lab_host="DH10B"
		/clone_1ib="NIH MGC 96"
		/note="Organ: brain; Vector: plasmidscriptR (modified pBluescript KS+); Site_1: BamHI Site_2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTGTATTTTTTTTIVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
	ORIGIN	
	Query Match	41.5%; Score 505.4; DB 12; Length 711;
	Best Local Similarity	99.8%; Pred. No. 8.7e-118;
	Matches	506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	451 AGAAGCTGCATTGGATGTCACCAATCCCTGTAGTAGTAAGTTGGGAATAAGCTTCG	510
Db	142 AAAAGCGCATTTGGATGTCACCAATCCCTGTAGTAGTAAGTTGGGAATAAGCTTCG	201
Db	511 AACTTCTTTGGCATTTCACTTGTTAAAAACAATATAGATGCAAAATTCCTCAATCCAGGT	570
Db	202 AACTTCTTTGGCATTTCACTTGTTAAAAACAATATAGATGCAAAATTCCTCAATCCAGGT	261
Db	571 TTGTAAAACAGTACTTGGAAAAGTGAATCTAACCTAAAGATCGTCTTGGTTGGGCCGT	630
Db	262 TATGAAAACAGTACTTGGAAAAGTGAATCTAACCTAAAGATCGTCTTGGTTGGGCCGT	321
Db	631 GTTCTTAGGAGACAGAGGCTTGGCCAGGAGTGTGTTGACTCTTGAAGAACAATAC	690
Db	322 GTTCTTAGGAGAGAGAGGCTTGGCCAGGAGTGTGTTGACTCTTGAAGAACAATAC	381
Db	691 CGACTTCCAGAGGAGTGAAGGAGGAGGCTCTACACATGAGGTAATTCCTGATCTGGCGAGA	750
Db	382 CCACTTCCAGAGGAGTGAAGGAGGAGGCTCTACACATGAGGTAATTCCTGATCTGGCGAGA	441
Db	751 TGACAGTGAACAGATGACAGTGTGACACCCACACAGCAACAGGCGGAGAAACATGTCAGT	810
Db	442 TGACAGTGAACAGATGACAGTGTGACACCCACACAGCAACAGGCGGAGAAACATGTCAGT	501
Db	811 ACCCACTGTCGACACAGAGGAGCAACACAGGAGCCTGTGCGCCACCAAGAGGAGGCGCG	870
Db	502 ACCCACTGTCGACACAGAGGAGCAACACAGGAGCCTGTGCGCCACCAAGAGGAGGCGCG	561
Db	871 AGGAGCTCATGAGCCAGAGAGAAACAAATATGATGGAGGCTAGTGTGACACACT	930

Db	Accession	Definition	Accession	Definition
Db	562	AGGACCTCCATGAGCGCAAGGAAAGAAACAAATGTTGATGGGTATGTTGGACACACT	621	
Qy	931	GGCAGTAAATACGCACTCTTGATGATA 957		
Db	622	GGCAGTAAATACGCACTCTTGATGATA 648		
RESULT 10				
LOCUS	BUI61287	835 bp	MRNA	linear
DEFINITION	AGENCOURT 7960449 NIH_MGC_72	Homo sapiens	cdna clone IMAGE:6166363	
ACCESSION	BUI61287			
VERSION	BUI61287.1	GI:22675197		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 835)			
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1998)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: ATCC/DCT/DTP			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLN at:			
	http://image.lnl.gov			
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	Average insert size 2 kb. Library constructed by Life			
	Technologies."			
ORIGIN				
Query Match	41.5%; Score 505.4; DB 13; Length 835;			
Best Local Similarity	99.8%; Pred. No. 9.2e-118;			
Matches	506; Conservative 0; Mismatches 1; Indels 0; Gaps 0			
Qy	451	AGAACTGCATGATGATGTCAGAAATCCCTGTAGTTGATGTAATGTGGGAATTAAGCTTCG	510	
Db	65	AAAATCGCATTTGATGATTCGCAAAATCCCTGTAGTTGATGTAATGTGGGAATTAAGCTTCG	124	
Qy	511	AACCTTTCTTTGGCATTCACTGTTTAAACAATATGATGCAAAATTCCTCACTCCAGGT	570	
Db	125	AACCTTTCTTTGGCATTCACTGTTTAAACAATATGATGCAAAATTCCTCACTCCAGGT	184	
Qy	571	TATGAAAACAGACTTGAAAACTGAAAACTAATTAATGATCGTCTTTGGTGGGCGGT	630	
Db	165	TATGAAAACAGACTTGAAAACTGAAAACTAATTAATGATCGTCTTTGGTGGGCGGT	244	
Qy	631	GTTCTTAAGCAGACAGAAAGCTTGGCAGAGGTCTGTTGATCTCGAAGAGACACATAGC	690	
Db	245	GTTCTTAAGCAGACAGAAAGCTTGGCAGAGGTCTGTTGATCTCGAAGAGACACATAGC	304	
Qy	691	CCACTTCCTAGGAGATGAGGTGCCGCTACTACCATGGGTAAATTCCTGTATCTGCCAGA	750	
Db	305	CCACTTCCTAGGAGATGAGGTGCCGCTACTACCATGGGTAAATTCCTGTATCTGCCAGA	364	

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QY 751 TGACAGTGGAAACAGATGACAGTGTGACACCCCAACAGCAAGCCGAGAGACAGTGCAGT 810
DB 365 TGACAGTGGAAACAGATGACAGTGTGACACCCCAACAGCAAGCCGAGAGACAGTGCAGT 424
QY 811 ACCCACTGCTGACACAGAGAGCCACACCGGAGCCCTGTTCGGCCACCAAGAGGGGCGG 870
DB 425 ACCCACTGCTGACACAGAGAGCCACACCGGAGCCCTGTTCGGCCACCAAGAGGGGCGG 484
QY 871 AGGACCTCATGAGCCAGAGGAGAAACAAATGTGATGGCTGTGATGGACACACT 930
DB 485 AGGACCTCATGAGCCAGAGGAGAAACAAATGTGATGGCTGTGATGGACACACT 544
QY 931 GGCAGTAATACGAGACTCTTGTAGATTA 957
DB 545 GGCAGTAATACGAGACTCTTGTAGATTA 571

RESULT 11
BUS00574 857 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCOURT 7859738 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:6108995
DEFINITION 5', mRNA sequence.
ACCESSION BUS00574
VERSION BUS00574.1 GI:22801691
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: NIMH/LOF
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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/clone_1lb="NIH_MGC_64"
/notes="Vector: pOTB7a; Site 1: Cent; Site 2: Scel. This
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kb. Size selection done at the National Institute of
Mental Health, NIH. Note: this is a NIH_MGC library."

ORIGIN
Query Match 41.5%; Score 505.4; DB 13; Length 857;
Best Local Similarity 99.8%; Pred. No. 9.3e-118; Indels 0; Gaps 0;
Matches 506; Conservative 0; Mismatches 1;

QY 451 AGAAGTGCATGATGATCCAGATCCCTGTAGTGTGATTAATGTTGGGATTAAGCTTCG 510
DB 106 AAAATCGCATGATGATCCAGATCCCTGTAGTGTGATTAATGTTGGGATTAAGCTTCG 165
QY 511 AACCTTCTTGGCATTCAGTGTGTTAAACCAATGATGCAAAATTCCTCAACTCCAGT 570
DB 166 AACCTTCTTGGCATTCAGTGTGTTAAACCAATGATGCAAAATTCCTCAACTCCAGT 225
QY 571 TTGAAAAACAGTACTGGAAAACTGAAATCTTAATGATCGCTTGGTGGGCGCT 630

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DB 226 TATGAAAAACAGTACTGGAAAACTGAAACTACTAATATGATCGCTTGTGGTGGCGCT 285
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DB 286 GTTCTTACGAGAGAGAGACCTTGGCCAGGGCTGTGTTGATCTCGAAGAGCATAGC 345
QY 691 CCACTTCTTACGAGAGAGAGTGTGCGCTTACTTACATATGGTAAATTCCTGATTCGCGAGA 750
DB 346 CCACTTCTTACGAGAGAGTGTGCGCGCTTACTTACATATGGTAAATTCCTGATTCGCGAGA 405
QY 751 TGACAGTGGAAACAGATGACAGTGTGACACCCCAACAGCAAGCCGAGAGACAGTGCAGT 810
DB 406 TGACAGTGGAAACAGATGACAGTGTGACACCCCAACAGCAAGCCGAGAGACAGTGCAGT 465
QY 811 ACCCACTGCTGACACAGAGAGCCACACCGGAGCCCTGTTCGGCCACCAAGAGGGGCGG 870
DB 466 ACCCACTGCTGACACAGAGAGCCACACCGGAGCCCTGTTCGGCCACCAAGAGGGGCGG 525
QY 871 AGGACCTCATGAGCCAGAGGAGAAACAAATGTGATGGCTGTGATGGACACACT 930
DB 526 AGGACCTCATGAGCCAGAGGAGAAACAAATGTGATGGCTGTGATGGACACACT 585
QY 931 GGCAGTAATACGAGACTCTTGTAGATTA 957
DB 586 GGCAGTAATACGAGACTCTTGTAGATTA 612

RESULT 12
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LOCUS AGENCOURT 7764766 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6013976
DEFINITION 5', mRNA sequence.
ACCESSION BQ439291
VERSION BQ439291.1 GI:21178367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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Location/Qualifiers
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/clone_1lb="NIH_MGC_92"
/notes="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN
Query Match 41.5%; Score 505.4; DB 13; Length 871;
Best Local Similarity 99.8%; Pred. No. 9.4e-118; Indels 0; Gaps 0;
Matches 506; Conservative 0; Mismatches 1;

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 DB 167 AACCTCTTTGGGATTCAGTGTGTAAACAAATAGATGCAAAATCTCACTCCAGGT 226
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 DB 227 TATGAAAACAGTACTGGAAACCTGAAATAGTGAATAGTGGGAATAGCTGCG 286
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 DB 287 GTTCTTAGGAG 346
 QY 691 CCACCTTCTTAGGAG 750
 DB 347 CCACCTTCTTAGGAG 406
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 DB 467 ACCCACTGCTGACACAG 526
 QY 871 AGGACCTCATGAG 930
 DB 527 AGGACCTCATGAG 586
 QY 931 GGCAGTATACGAGACTCTTGTAGATGA 957
 DB 587 GGCAGTATACGAGACTCTTGTAGATGA 613

RESULT 13

LOCUS CD683922 670 bp mRNA linear EST 25-JUN-2003
 DEFINITION EST1442 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD683922
 VERSION CD683922.1 GI:32198428

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 670)
 Liu, X.-Q., Zhou, Y., Zhang, D.-D., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.
 Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)
 CONTACT: Yixin Zeng

ORGANISM
 Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510660, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506

Email: yxzeng@gzsun.edu.cn.
 Location/Qualifiers

FEATURES

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Best Local Similarity 99.6%; Pred. No. 2,2e-117;
 Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 266 TATGAAAACAGTACTGGAAACCTGAAATAGTGAATAGTGGGAATAGCTGCG 325
 QY 631 GTTCTTAGGAG 690
 DB 326 GTTCTTAGGAG 385
 QY 691 CCACCTTCTTAGGAG 750
 DB 386 CCACCTTCTTAGGAG 445
 QY 751 TGACAGTGGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
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 QY 811 ACCCACTGCTGACACAG 870
 DB 506 ACCCACTGCTGACACAG 565
 QY 871 AGGACCTCATGAG 930
 DB 566 AGGACCTCATGAG 625
 QY 931 GGCAGTATACGAGACTCTTGTAGATGA 957
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RESULT 14

LOCUS BG749354 727 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602707829F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844622 5',
 mRNA sequence.
 ACCESSION BG749354
 VERSION BG749354.1 GI:14060007

KEYWORDS EST.
 SOURCE Homo sapiens (human)

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 727)
 NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: c9abps-remail.nih.gov

ORGANISM
 CDNA Library Preparation: ATCC

CDNA Library Preparation: ATCC
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
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 Note: this is a NIH_MGC Library."

ORIGIN

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 Best Local Similarity 99.6%; Pred. No. 2.4e-117; Indels 0; Gaps 0;
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 511 AACTTCTTGGCATGTCAGTTGTAATAAACAATAGATGCAATTCCTCACTCCAGGT 570
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 333 GTTCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 392
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 393 CCACCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 452
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 453 TGAAGTGGAAACAGATGACATGTTGACACCCACACGAGCCAGAAACAGTGAAGT 512
 811 ACCCACTGCTGACACAGAGAGCCACACGAGCCCTGTTGCGGACCAACAGAGGCGCG 870
 513 ACCCACTGCTGACACAGAGAGCCACACGAGCCCTGTTGCGGACCAACAGAGGCGCG 572
 871 AGAAGCTCATAGGCGAAGAGAAACAAATATGATGAGTGGCTAGTGTGGACACACT 930
 573 AGAAGCTCATAGGCGAAGAGAAACAAATATGATGAGTGGCTAGTGTGGACACACT 632
 931 GGAGTAATACGAGACTTGTGATTA 957
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RESULT 15
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 LOCUS 603299714.F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:531398 5',
 DEFINITION mRNA sequence.
 ACCESSION B1668768
 VERSION B1668768.1 GI:15583001
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rstraus@nigms.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone Genotyping: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
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 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 41.4%; Score 503.8; DB 12; Length 834;
 Best Local Similarity 99.6%; Pred. No. 2.4e-117; Indels 0; Gaps 0;
 Matches 505; Conservative 0; Mismatches 2;

451 AGAAGCTGCATGATGTCAGAAATCCCTGTAGTTAATATGTTGGAAATAGCTCTGC 510
 142 AAAAGTGCATGATGTCAGAAATCCCTGTAGTTAATATGTTGGAAATAGCTCTGC 201
 511 AACTTCTTGGCATGTCAGTTGTAATAAACAATAGATGCAATTCCTCACTCCAGGT 570
 202 AACTTCTTGGCATGTCAGTTGTAATAAACAATAGATGCAATTCCTCACTCCAGGT 261
 571 TATGAAAACAGTACTTGGAAAACCTGAAATCTAAATATGATCGTCTTTGGTGGCCGT 630
 262 TATGAAAACAGTACTTGGAAAACCTGAAATCTAAATATGATCGTCTTTGGTGGCCGT 321
 631 GTTCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 690
 322 GTTCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 381
 691 CCACCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 750
 382 CCACCTTCCAGGAGAGAGCCCTGGCCAGGCTCTGTTGATCTCTGAAAGACATAGC 441
 751 TGAAGTGGAAACAGATGACATGTTGACACCCACACGAGCCAGAAACAGTGAAGT 810
 442 TGAAGTGGAAACAGATGACATGTTGACACCCACACGAGCCAGAAACAGTGAAGT 501
 811 ACCCACTGCTGACACAGAGAGCCACACGAGCCCTGTTGCGGACCAACAGAGGCGCG 870
 502 ACCCACTGCTGACACAGAGAGCCACACGAGCCCTGTTGCGGACCAACAGAGGCGCG 561
 871 AGAAGCTCATAGGCGAAGAGAAACAAATATGATGAGTGGCTAGTGTGGACACACT 930
 562 AGAAGCTCATAGGCGAAGAGAAACAAATATGATGAGTGGCTAGTGTGGACACACT 621
 931 GGAGTAATACGAGACTTGTGATTA 957
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PR	26-OCT-1998;	98US-01056533P
PR	26-OCT-1998;	98US-01056544P
PR	27-OCT-1998;	98US-01058077P
PR	27-OCT-1998;	98US-01058811P
PR	27-OCT-1998;	98US-01058822P
PR	27-OCT-1998;	98US-01060622P
PR	28-OCT-1998;	98US-01060623P
PR	28-OCT-1998;	98US-01060299P
PR	28-OCT-1998;	98US-01060309P
PR	28-OCT-1998;	98US-01060322P
PR	28-OCT-1998;	98US-01060332P
PR	28-OCT-1998;	98US-01061788P
PR	29-OCT-1998;	98US-01065248P
PR	29-OCT-1998;	98US-01065384P
PR	29-OCT-1998;	98US-01065390P
PR	30-OCT-1998;	98US-01064640P

PR	03-NOV-1998	98US-0106856P
PR	03-NOV-1998	98US-0106902P
PR	03-NOV-1998	98US-0106952P
PR	03-NOV-1998	98US-0106931P
PR	03-NOV-1998	98US-0106932P
PR	03-NOV-1998	98US-0106934P
PR	10-NOV-1998	98US-0107783P
PR	17-NOV-1998	98US-0108775P
PR	17-NOV-1998	98US-0108779P
PR	17-NOV-1998	98US-0108787P
PR	17-NOV-1998	98US-0108788P
PR	17-NOV-1998	98US-0108801P
PR	17-NOV-1998	98US-0108802P
PR	17-NOV-1998	98US-0108806P
PR	17-NOV-1998	98US-0108807P
PR	17-NOV-1998	98US-0108867P
PR	17-NOV-1998	98US-0108925P
PR	18-NOV-1998	98US-0108848P
PR	18-NOV-1998	98US-0108849P
PR	18-NOV-1998	98US-0108850P
PR	18-NOV-1998	98US-0108851P
PR	18-NOV-1998	98US-0108852P
PR	18-NOV-1998	98US-0108853P
PR	18-NOV-1998	98US-0108904P

(GETH) GENENTECH INC

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI, ...

WPI; 2000-237871/20

P-PSDB; AAY99341

PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.

Claim 2; Fig 3; 773pp; English.

CC AA337322 to AA3714 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AA593140 to AA59462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AA37245 to AA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention

SD Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match	100.0%; Score 1218; DB 3; Length 1218;
-------------	--

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACA 60

b 1 CCCACGCGTCCGGCGCGCTCGCCCTCCGCTCCATCTTTGCCGTTCTCTCGGACCTGTACA 60

61 AAGGAGTCGCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGAGGTAGAGAACT 12

b 61 AAGGAGTCGCGCCGCGCCGCCCCCTCCCTCCGGTGGCCCGGAGGTAGAGAAAGT 12

121 CAGTGCACAGCCCGACCGCTGCTCTGAGCCCTGGCACCGCGAACGGAGGAGTCT 18

121 CAGTGCACAGCCCGACCGGCTGCTCTGAGCCCTGGCAACGGGAACGGAGGAGTCT 18

181 GAGGTTGGGACGCTGTGAGCGAGGGGAACAGCCGCTCGAGCCTGGGGCGCGGACC 24

181 GAGGTTGGGACGTCGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGGACC 241

241 GGACTGGGCCGGGTAGCTCTGGAAGGCCCGGAGAGAGGTGGCGTGTGTCAGAAC 300

241 GGA CTGGG CCGG GTAG CTCTG GAAAG GCGCC CGGAG AGAGT GCGCT TGTCA GAAC 300

```

QY 301 CTGAGAAACAGCCGAGAGGTTTTCACCGAGGCCGCGCTTGAAGGATCTGAAGGTTTC 360
DB 301 CTGAGAAACAGCCGAGAGGTTTTCACCGAGGCCGCGCTTGAAGGATCTGAAGGTTTC 360
QY 361 CTGAGAAAGAGGTTTCCCTCTTCCGAGGAGCTTCAACAGAGGTTCTTGAGGAGGTC 420
DB 361 CTGAGAAAGAGGTTTCCCTCTTCCGAGGAGCTTCAACAGAGGTTCTTGAGGAGGTC 420
QY 421 CTCTGAGAGGCTGCGGCTTACAGAGGCCAGAACTGCGATTGATGTCAGAAATCCCT 480
DB 421 CTCTGAGAGGCTGCGGCTTACAGAGGCCAGAACTGCGATTGATGTCAGAAATCCCT 480
QY 481 GTAGTTGATTAATGTTGGAAATAGCTCTGCAACTCTTCTTGAGATCACTGTTAAAG 540
DB 481 GTAGTTGATTAATGTTGGAAATAGCTCTGCAACTCTTCTTGAGATCACTGTTAAAG 540
QY 541 AATAGGATGCAAAATTCCTCACTCCAGGTTATGAAACAGTACTGAAACTGAAAC 600
DB 541 AATAGGATGCAAAATTCCTCACTCCAGGTTATGAAACAGTACTGAAACTGAAAC 600
QY 601 TACCTAATATGATGCTCTTGGTGGGCGCTTCTTGAAGAGAGAGGCTTGCGAGG 660
DB 601 TACCTAATATGATGCTCTTGGTGGGCGCTTCTTGAAGAGAGAGGCTTGCGAGG 660
QY 661 TCTGTTGTTGACTCTCGAAGAGCACAATAGCCCACTTCTTGAAGAGAGGCTTGCG 720
DB 661 TCTGTTGTTGACTCTCGAAGAGCACAATAGCCCACTTCTTGAAGAGAGGCTTGCG 720
QY 721 TACCATGGGTAATCTCTGTAATCTGCGGAGATGACAGTGAACAGATGACAGTGT 780
DB 721 TACCATGGGTAATCTCTGTAATCTGCGGAGATGACAGTGAACAGATGACAGTGT 780
QY 781 CCAACAGCAACAGGCGGAGAAAGTGCAGTACCCTGCTGACACAGAGAGGAGCAAC 840
DB 781 CCAACAGCAACAGGCGGAGAAAGTGCAGTACCCTGCTGACACAGAGAGGAGCAAC 840
QY 841 GGACCCCTGTTCCGACCAAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GGACCCCTGTTCCGACCAAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 AAAAGTGAAGGAGGAGTGAAGTGAACACAGTGGAGTAACTCGGACTCTTGAAGTA 960
DB 901 AAAAGTGAAGGAGGAGTGAAGTGAACACAGTGGAGTAACTCGGACTCTTGAAGTA 960
QY 961 AGTATCTGACTCAGGTCACCTCCAGTGAATGAAAGTGTCTGCGGAGCACTGACT 1020
DB 961 AGTATCTGACTCAGGTCACCTCCAGTGAATGAAAGTGTCTGCGGAGCACTGACT 1020
QY 1021 TTAGGACTCTTCCAGTCTCTTGAAGATCTGCGCAAGGCTTGTGCTCAGGAGCAAG 1080
DB 1021 TTAGGACTCTTCCAGTCTCTTGAAGATCTGCGCAAGGCTTGTGCTCAGGAGCAAG 1080
QY 1081 GAGAAATTTTAAATGCTCCGCTGATGAGAGTAAATGATTAAGATTGATGTTTGGT 1140
DB 1081 GAGAAATTTTAAATGCTCCGCTGATGAGAGTAAATGATTAAGATTGATGTTTGGT 1140
QY 1141 GCTGTGATCTACTTGTGCTGAAGATGCTTAATGTTCTGTAAGAGAAACAGATAAG 1200
DB 1141 GCTGTGATCTACTTGTGCTGAAGATGCTTAATGTTCTGTAAGAGAAACAGATAAG 1200
QY 1201 CTATGATCTTATTAAG 1218
DB 1201 CTATGATCTTATTAAG 1218

```

```

RESULT 2
AAFS4205
ID AAFS4205 standard; DNA; 1218 BP.
AC AAFS4205;
XX
DT 02-APR-2001 (first entry)

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XX DNA encoding protein of the invention #2.
DE Secreted; transmembrane; gene therapy; ss.
XX
XX Unidentified.
XX
XX MO200078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 29-OCT-1999; 98US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US030095.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX
XX (GENTH ) GENEVENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AB, Hillan KJ,
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX
XX WPI, 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 2; Fig 3; 787p; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX CC These proteins and the DNA encoding them may be used as hybridization
XX CC probes, in chromosome and gene mapping and in the generation of anti-
XX CC sense RNA and DNA. They may also be used used to generate either
XX CC transgenic animals or knockout animals which are in turn useful for
XX CC development and screening of therapeutically useful reagents. The nucleic
XX CC acids may also be used in gene therapy
XX
XX Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 1218; DB 4; Length 1218;
XX Best local Similarity 100.0%; Pred. No. 0;
XX Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 CTGAGAAACAGCCGAGAGGTTTTCACCGAGGCCGCGCTTGAGGGATCTGAAGAGGTTT 360
DB 301 CTGAAACACGCGAGAGGTTTTCACCGAGGCCGCGCTTGAGGGATCTGAAGAGGTTT 360
QY 361 CTGAAAGAGGAGTGTTCCTCTTTTCGAGGAGTCTCAACGAAAGAGTGTTCGAGGAGT 420
DB 361 CTGAAAGAGGAGTGTTCCTCTTTTCGAGGAGTCTCAACGAAAGAGTGTTCGAGGAGT 420
QY 421 CTTCTGAGAGAGGCTGCGGTATACAGAGGCCGAGAACTGCAATGATGATGATGATGAT 480
DB 421 CTTCTGAGAGAGGCTGCGGTATACAGAGGCCGAGAACTGCAATGATGATGATGATGAT 480
QY 481 GTAGTTGATATAGTTGGGAAATAGCTTCGCACTTTCTTTGGCATTCAGTTGTTAAAAA 540
DB 481 GTAGTTGATATAGTTGGGAAATAGCTTCGCACTTTCTTTGGCATTCAGTTGTTAAAAA 540
QY 541 AAATAGGATGCAAAATTTCTCTCACTCGAGGTTATGAAAAAGATGATGATGATGATGAT 600
DB 541 AAATAGGATGCAAAATTTCTCTCACTCGAGGTTATGAAAAAGATGATGATGATGATGAT 600
QY 601 TACCTTAATGATCGATTTGTTGGGCGCTGTTCTTAGCGAGCAGAACCTTTGGCGAGG 660
DB 601 TACCTTAATGATCGATTTGTTGGGCGCTGTTCTTAGCGAGCAGAACCTTTGGCGAGG 660
QY 661 TCTGTTGTTGACTCTCGAAGAGACATAGCCCACTTCTTAGGAGCTGAGAGTGCCTAC 720
DB 661 TCTGTTGTTGACTCTCGAAGAGACATAGCCCACTTCTTAGGAGCTGAGAGTGCCTAC 720
QY 721 TACCATGAGTAAATCTGATATGCGGAGATGACAGTGAACAGATGACAGTGTGACAC 780
DB 721 TACCATGAGTAAATCTGATATGCGGAGATGACAGTGAACAGATGACAGTGTGACAC 780
QY 781 CCAACAGCAACAGGCGGAGAAACAGTGCATCCACTGCTGACACAGAGCCACACAC 840
DB 781 CCAACAGCAACAGGCGGAGAAACAGTGCATCCACTGCTGACACAGAGCCACACAC 840
QY 841 GAGCCCTGTTGCGGCAACAGAGAGGCGGAGAGCTCATGAGCCAGAGAAAGAAACA 900
DB 841 GAGCCCTGTTGCGGCAACAGAGAGGCGGAGAGCTCATGAGCCAGAGAAAGAAACA 900
QY 901 AAATGATGATGAGGCTAGTGTGACACACTGCGAGTAATAGAGTCTTTGATGATAGTA 960
DB 901 AAATGATGATGAGGCTAGTGTGACACACTGCGAGTAATAGAGTCTTTGATGATAGTA 960
QY 961 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TTAGGACTCCTTCACTTCTTTAGGACATATCTGCCAGCCTTGTGCTCACAGGCAAG 1080
DB 1021 TTAGGACTCCTTCACTTCTTTAGGACATATCTGCCAGCCTTGTGCTCACAGGCAAG 1080
QY 1081 GAGAAATATTTAATGCTCCGCTGATGAGCAGAGTAATGATGATGATGATGATGATGAT 1140
DB 1081 GAGAAATATTTAATGCTCCGCTGATGAGCAGAGTAATGATGATGATGATGATGATGAT 1140
QY 1141 GCTGCTATCTACTTGTGCTGGAATGCTTAATGTTTCTGTAGCAGAAAAACGATTAAG 1200
DB 1141 GCTGCTATCTACTTGTGCTGGAATGCTTAATGTTTCTGTAGCAGAAAAACGATTAAG 1200
QY 1201 CTATGATCTTTATTAGG 1218
DB 1201 CTATGATCTTTATTAGG 1218

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RESULT 3
AAC86965
ID AAC86965 standard; cDNA; 1218 BP.
XX
XX AAC86965;
XX
XX 20-APR-2001 (first entry)
XX

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DE Nucleotide sequence of human polypeptide PRO444.
XX
XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO196; PRO210; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO333; PRO301; PRO187; PRO371; PRO4356;
KW PRO246; PRO265; PRO941; PRO1096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 608..961
XX sig_peptide /tag= a
XX FT 608..655
XX FT /tag= b
XX EN
XX
XX 21-DEC-2000.
XX
XX 22-MAY-2000; 2000MO-US014042.
XX
XX 15-JUN-1999; 99US-0139695P.
XX 20-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145698P.
XX 17-AUG-1999; 99US-0149396P.
XX 01-SEP-1999; 99MO-US020111.
XX 08-SEP-1999; 99MO-US020594.
XX 15-SEP-1999; 99MO-US021090.
XX 15-SEP-1999; 99MO-US021547.
XX 30-NOV-1999; 99MO-US028313.
XX 01-DEC-1999; 99MO-US028301.
XX 02-DEC-1999; 99MO-US028365.
XX 07-DEC-1999; 99US-0169495P.
XX 05-JAN-2000; 2000MO-US000219.
XX 18-FEB-2000; 2000MO-US004341.
XX 18-FEB-2000; 2000MO-US004342.
XX 22-FEB-2000; 2000MO-US004414.
XX 01-MAR-2000; 2000MO-US005601.
XX 02-MAR-2000; 2000MO-US005641.
XX 20-MAR-2000; 2000MO-US007377.
XX 30-MAR-2000; 2000MO-US008439.
XX 15-MAY-2000; 2000MO-US013358.
XX 17-MAY-2000; 2000MO-US013705.
XX
XX (GENE) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers J, Eaton DL,
XX Ferrarese N, Fong S, Geo W, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Guirney AJ, Kljavin IJ, Macher JP, Napier MA, Pan J,
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
XX Wood WT, Zhang Z;
XX
XX WPI; 2001-050091/06.
XX P-PDB; AAB31180.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
XX transmembrane polypeptide is useful for gene therapy and identification
XX of related polypeptides.
XX
XX Claim 2; Fig 3; 244pp; English.
XX
XX The present sequence encodes a human secreted and transmembrane
XX polypeptide. The specification describes human polypeptides, designated
XX PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO4999, PRO7170,
XX PRO248, PRO353, PRO333, PRO301, PRO187, PRO371, PRO4356,
XX PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO1096, PRO6003,
XX PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
XX can be modulated with agents that bind to these polypeptides, resulting
XX in the death of the cells. The polynucleotides encoding these

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CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene

XX Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 4; Length 1218;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCACGGGCTCCGGGCGCGCTGCGCTCCATCTTGGCCGTTCTCCCGACCTGTCA 60
D 1 CCCACGGGCTCCGGGCGCGCTGCGCTCCATCTTGGCCGTTCTCCCGACCTGTCA 60
QY 61 AAGGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
D 61 AAGGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 CAGTGCACACCCCGACCGCGCGCTCTGTAGCCCTGGGCGACCGGGAACGGAGTCT 180
D 121 CAGTGCACACCCCGACCGCGCGCTCTGTAGCCCTGGGCGACCGGGAACGGAGTCT 180
QY 181 GAGGCTTGGGCGACCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 240
D 181 GAGGCTTGGGCGACCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 240
QY 241 GGAGCTGGGCGCGCGCGCTGTGAAAAGGCGCGGAGAGAGAGAGAGAGAGT 300
D 241 GGAGCTGGGCGCGCGCGCTGTGAAAAGGCGCGGAGAGAGAGAGAGAGT 300
QY 301 CTGAGAAACAGCGAGAGAGTTCACCGAGAGCGCGCGCTTGAAGAGATCGAAGAGT 360
D 301 CTGAGAAACAGCGAGAGAGTTCACCGAGAGCGCGCGCTTGAAGAGATCGAAGAGT 360
QY 361 CTAGAAAGAGGAGTTCCTCTTGGGGGCTCTTCAACAGAGAGAGTCTTGGGAGT 420
D 361 CTAGAAAGAGGAGTTCCTCTTGGGGGCTCTTCAACAGAGAGAGTCTTGGGAGT 420
QY 421 CTCTGAGAGAGCGCGCGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGT 480
D 421 CTCTGAGAGAGCGCGCGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGT 480
QY 481 GTAGTGAATATGTTGGGAATAGCTGTCAACTTTCTTTGGCATTCAGTTGTTAA 540
D 481 GTAGTGAATATGTTGGGAATAGCTGTCAACTTTCTTTGGCATTCAGTTGTTAA 540
QY 541 AAATAGATGCAAAATCTCTCACTCCAGGTATGAAAACAGTACTTGGAAAAC 600
D 541 AAATAGATGCAAAATCTCTCACTCCAGGTATGAAAACAGTACTTGGAAAAC 600
QY 601 TACCTAAATGATCGCTTGTGGGCGGTGTCTTAGCGAGAAAGCCTTGGCCAGG 660
D 601 TACCTAAATGATCGCTTGTGGGCGGTGTCTTAGCGAGAAAGCCTTGGCCAGG 660
QY 661 TACCTAAATGATCGCTTGTGGGCGGTGTCTTAGCGAGAAAGCCTTGGCCAGG 660
D 661 TACCTAAATGATCGCTTGTGGGCGGTGTCTTAGCGAGAAAGCCTTGGCCAGG 660
QY 720 TCTGTTGTTGACTCTGAAAGAGACATAGCCCACTTCTTAGGAGCTGAGAGTCCG 720
D 720 TCTGTTGTTGACTCTGAAAGAGACATAGCCCACTTCTTAGGAGCTGAGAGTCCG 720
QY 780 TACCATGGGTATTTCTGTATCTGCGAGATGACAGTGAACAGATGACATGTTGAC 780
D 780 TACCATGGGTATTTCTGTATCTGCGAGATGACAGTGAACAGATGACATGTTGAC 780
QY 780 TACCATGGGTATTTCTGTATCTGCGAGATGACAGTGAACAGATGACATGTTGAC 780
D 780 TACCATGGGTATTTCTGTATCTGCGAGATGACAGTGAACAGATGACATGTTGAC 780
QY 840 CCAACAGCAACAGCGCGAGAACAGTGCATGCCCTGCTGACACAGAGCCCAAC 840
D 840 CCAACAGCAACAGCGCGAGAACAGTGCATGCCCTGCTGACACAGAGCCCAAC 840
QY 900 GGAACCTGTTGGGCGACCAAGAGAGGCGCGAGAGCTCATAGGCCAAGAGAAACA 900
D 900 GGAACCTGTTGGGCGACCAAGAGAGGCGCGAGAGCTCATAGGCCAAGAGAAACA 900

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QY 901 AAATGTGATGAGGCTAGGTTGACACACACTGGCAGTAATACGACTCTTGTAGTA 960
D 901 AAATGTGATGAGGCTAGGTTGACACACACTGGCAGTAATACGACTCTTGTAGTA 960
QY 961 AGATATCTACTCAGCGGTCACTCCAGTGGAAATGAAAGTGTTCGCCGGAACCA 1020
D 961 AGATATCTACTCAGCGGTCACTCCAGTGGAAATGAAAGTGTTCGCCGGAACCA 1020
QY 1021 TTAGACATCTTCACTGCTTCTTAGACATATCGCAAGCCTTGTGCTCACAGG 1080
D 1021 TTAGACATCTTCACTGCTTCTTAGACATATCGCAAGCCTTGTGCTCACAGG 1080
QY 1081 GAGAAATATTTAATGCTCCGCTGATGCGAGAGTAATGATTAAGATTGATG 1140
D 1081 GAGAAATATTTAATGCTCCGCTGATGCGAGAGTAATGATTAAGATTGATG 1140
QY 1141 GCTGTATCTACTTGTCTGGAAGATGCTAATGTTCTGTAGAGAAAAACAG 1200
D 1141 GCTGTATCTACTTGTCTGGAAGATGCTAATGTTCTGTAGAGAAAAACAG 1200
QY 1201 CTATGATCTTTATTAAG 1218
D 1201 CTATGATCTTTATTAAG 1218

```

RESULT 4
 ABL8074
 ID ABL8074 standard; cDNA; 1218 BP.
 XX
 AC ABL8074;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO444 cDNA sequence SEQ ID NO:5.
 XX
 XX Human; angiodenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KM vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiotensin receptor; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 XX 23-JUN-2000; 2000US-0213637P.
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 25-JUL-2000; 2000US-0220644P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 02-AUG-2000; 2000US-0222695P.
 XX 17-AUG-2000; 2000US-0064657.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 07-SEP-2000; 2000US-0230978P.
 XX 18-SEP-2000; 2000US-00664610.
 XX 18-SEP-2000; 2000US-00665350.
 XX 24-OCT-2000; 2000US-0242922P.
 XX 08-NOV-2000; 2000US-00709328.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 20-DEC-2000; 2000WO-US034956.
 XX 22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-MAR-2001; 2001MO-US006520.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00806889.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854289.
 PR 10-MAY-2001; 2001US-00854289.
 PR 25-MAY-2001; 2001US-00860028.
 PR 25-MAY-2001; 2001US-00860028.
 PR 25-MAY-2001; 2001US-00860028.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 (GETH) GENENTECH INC.
 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PK, Wood WI, Ye W,
 XX
 DR WFI: 2002-090516/12.
 DR P-PSDB; ABB84819.
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 2; Fig 5; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1218; DB 6; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

301 CTGAGAAACAGCGGAGAGGTTTCCACCGAGGCCCGCGCTTAGGAGATCTGAAGAGTTTC 360
 Db
 QY 361 CTGAGAAAGAGGTTTCCCTCTTTGGGGGGTCTTCAACCAAGAAAGTTCTGGGGGGTCCGC 420
 QY 361 CTGAGAAAGAGGTTTCCCTCTTTGGGGGGTCTTCAACCAAGAAAGTTCTGGGGGGTCCGC 420
 Db
 QY 421 CTCTGAGAGAGGTTGCGGCTTAACAGAGGCCAGAACTGCAATTTGATGTCAGAAATCCCT 480
 Db 421 CTCTGAGAGAGGTTGCGGCTTAACAGAGGCCAGAACTGCAATTTGATGTCAGAAATCCCT 480
 QY 481 GATGTTGATATGTTGGGAAATTAAGCTTTCGAATTTCTTGGCATTCAGTTGTTAAAC 540
 Db 481 GATGTTGATATGTTGGGAAATTAAGCTTTCGAATTTCTTGGCATTCAGTTGTTAAAC 540
 QY 541 AAATAGAGTCAATTCCTCAACTCCAGGTTTGAAGAAAGTACTTGAAGAACTGAAAC 600
 Db 541 AAATAGAGTCAATTCCTCAACTCCAGGTTTGAAGAAAGTACTTGAAGAACTGAAAC 600
 QY 601 TACCTAATGATGCTTTGGTTGGGCGGTGTTTTCAGGAGCAAGGCTTTGGCCAGG 660
 Db 601 TACCTAATGATGCTTTGGTTGGGCGGTGTTTTCAGGAGCAAGGCTTTGGCCAGG 660
 QY 661 TCTGTTGTTGACTCTGAGAGAGCAATAGCCCACTTCTAGGAGCTGAGAGTGGCTTAC 720
 Db 661 TCTGTTGTTGACTCTGAGAGAGCAATAGCCCACTTCTAGGAGCTGAGAGTGGCTTAC 720
 QY 721 TACCATGGTAAATTCCTGATATCTGCGAGATGACATGAGAAAGATGACATGTTGACAC 780
 Db 721 TACCATGGTAAATTCCTGATATCTGCGAGATGACATGAGAAAGATGACATGTTGACAC 780
 QY 781 CCAAGCAACAGCGGAGAGAAAGTCACTGATCCCACTGTCACAAAGAGCAACCAAG 840
 Db 781 CCAAGCAACAGCGGAGAGAAAGTCACTGATCCCACTGTCACAAAGAGCAACCAAG 840
 QY 841 GGAACCTGTTGGGCAACCAAGAGGGCCGAGAGCTCTATGACCAAGAGAAAGAAACA 900
 Db 841 GGAACCTGTTGGGCAACCAAGAGGGCCGAGAGCTCTATGACCAAGAGAAAGAAACA 900
 QY 901 AAATGAGAGGCTAGTGTGACACACTGAGGATTAACGATCTTGTGATTAAGTA 960
 Db 901 AAATGAGAGGCTAGTGTGACACACTGAGGATTAACGATCTTGTGATTAAGTA 960
 QY 961 AGTATGATCACTGAGGATCACTCAAGTGAATGAAGTGTCTGCGGAAACCATGACT 1020
 Db 961 AGTATGATCACTGAGGATCACTCAAGTGAATGAAGTGTCTGCGGAAACCATGACT 1020
 QY 1021 TTAGGACTCTTCACTTCTTTAGGACATTAATCTGCAAGCTTTGTCTCAAGGGCAAG 1080
 Db 1021 TTAGGACTCTTCACTTCTTTAGGACATTAATCTGCAAGCTTTGTCTCAAGGGCAAG 1080
 QY 1081 GAGAAATTTTAATGCTCCGCTGATGAGAGAGTAATGATTAAGTTGTTTGGCTT 1140
 Db 1081 GAGAAATTTTAATGCTCCGCTGATGAGAGAGTAATGATTAAGTTGTTTGGCTT 1140
 QY 1141 GCTGTCACTCACTTGTCTGGAATGCTTAATGTTTCTGTAGCAAGAAACAGATTAAG 1200
 Db 1141 GCTGTCACTCACTTGTCTGGAATGCTTAATGTTTCTGTAGCAAGAAACAGATTAAG 1200
 QY 1201 CTATGATCTTTATTAAG 1218
 Db 1201 CTATGATCTTTATTAAG 1218

RESULT 5
 ABL95563
 ID ABL95563 standard; cDNA; 1218 BP.
 XX
 AC ABL95563;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Human angiogenesis related cDNA PRO444 SEQ ID NO: 5.

QY 781 CCACAGCAAGGCGCCAGAACAGTGCAGTACCCACTGCTGCACACAGAGCCACACAG 840
DB 781 CCAACAGCAAGGCGCCAGAACAGTGCAGTACCCACTGCTGCACACAGAGCCACACAG 840
QY 841 GGACCCCTGTCGCGCCACCAAGAGAGGCGCCAGACCTCATGACCAAGAGAAAGAAACA 900
DB 841 GGACCCCTGTCGCGCCACCAAGAGAGGCGCCAGACCTCATGACCAAGAGAAAGAAACA 900
QY 901 AAATGTGATGGGTAGTGTGACACACTGGAGTAATCGACCTCTGTAGATAAGTA 960
DB 901 AAATGTGATGGGTAGTGTGACACACTGGAGTAATCGACCTCTGTAGATAAGTA 960
QY 961 AGTATCTGACTCAGGCTCAGCTCCAGTGAATGAAAGTTTGCCTCCGGAACATGACT 1020
DB 961 AGTATCTGACTCAGGCTCAGCTCCAGTGAATGAAAGTTTGCCTCCGGAACATGACT 1020
QY 1021 TTAGACCTCTTCAGTCTCTTTAGACATACCTGCGCCAGCTGTGCTCAAGGCGAAG 1080
DB 1021 TTAGACCTCTTCAGTCTCTTTAGACATACCTGCGCCAGCTGTGCTCAAGGCGAAG 1080
QY 1081 GAGAAATATTTAATGCTCCGCTGATGCGCAGATGAATGATGATTTGTTTCTT 1140
DB 1081 GAGAAATATTTAATGCTCCGCTGATGCGCAGATGAATGATGATTTGTTTCTT 1140
QY 1141 GCTGTGATCTCTCTTTGCTGGAATGTCTAAATGTTTCTGTAGACAAAACGATTAAG 1200
DB 1141 GCTGTGATCTCTCTTTGCTGGAATGTCTAAATGTTTCTGTAGACAAAACGATTAAG 1200
QY 1201 CTATGATCTTTATTAGAG 1218
DB 1201 CTATGATCTTTATTAGAG 1218
RESULT 6
ACD42316
ID ACD42316 standard; cDNA; 1218 BP.
XX
AC ACD42316;
XX
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; anti-diabetic;
KW opthalmo; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063339P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98US-00814552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0018624.
PR 14-SEP-1998; 98US-0018093.
PR 16-SEP-1998; 98US-0019330.
PR 17-SEP-1998; 98US-0100888P.
PR 24-SEP-1998; 98US-01019437.
PR 28-OCT-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-0024855.
PR 25-NOV-1998; 98US-0025190.
PR 01-DEC-1998; 98US-0025108.
PR 08-MAR-1999; 99US-00505028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99US-0125778P.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145598P.
PR 17-AUG-1999; 99US-0149596P.
PR 01-SEP-1999; 99US-0020111.
PR 08-SEP-1999; 99US-0020594.
PR 15-SEP-1999; 99US-0021090.
PR 30-NOV-1999; 99US-0021547.
PR 01-DEC-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028301.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99US-0030999.
PR 05-JAN-2000; 2000US-0000219.
PR 18-FEB-2000; 2000US-0004341.
PR 18-FEB-2000; 2000US-0004342.
PR 22-FEB-2000; 2000US-0004414.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005841.
PR 09-MAR-2000; 2000US-0005471.
PR 20-MAR-2000; 2000US-0007377.
PR 30-MAR-2000; 2000US-0008439.
PR 15-MAY-2000; 2000US-0013358.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 11-AUG-2000; 2000US-0022031.
PR 23-AUG-2000; 2000US-0023522.
PR 24-AUG-2000; 2000US-0023528.
PR 01-DEC-2000; 2000US-0032678.
PR 28-FEB-2001; 2001US-0006520.
PR 30-MAY-2001; 2001US-0017443.
PR 01-JUN-2001; 2001US-0017800.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 15-NOV-2001; 2001US-00002796.
(GENTH) GENENTECH INC.
XX
PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DJ,
PI Ferrara NJ, Fong S, Gao W, Gerber H, Gertsen ME, Goddard A,
PI Godowski PJ, Guirney AL, Kijavits ID, Mather JP, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX
XX WPI; 2003-503396/47.
XX P-PSDB; ABO25151.


```

Db      421  |||||CTTCTGAGGAGCGCGCTTAACAGGGCCAGAACTGCCATTCGATGTCAGATCCCT 480
Qy      481  |||||GTAGTTATATATGTTGGGAATTAAGCTTCGCAACTTTCTTTGGCATTGAGTTTAAAC 540
Db      481  |||||GTAGTTATATATGTTGGGAATTAAGCTTCGCAACTTTCTTTGGCATTGAGTTTAAAC 540
Qy      541  |||||AAATGAGATGCAAAATTCCTCACTCCAGGTTATGAAAAAGCTACTTGGAAAACTGAAAC 600
Db      541  |||||AAATGAGATGCAAAATTCCTCACTCCAGGTTATGAAAAAGCTACTTGGAAAACTGAAAC 600
Qy      601  |||||TACCTAATATGATGCTCTTTGGTGGGCGGTTCTTTCAGCAGAGAAAGCTTGGCAGAG 660
Db      601  |||||TACCTAATATGATGCTCTTTGGTGGGCGGTTCTTTCAGCAGAGAAAGCTTGGCAGAG 660
Qy      661  |||||TCTGTTGTGACCTCTCGAAGAGCAGATAGCCCACTTCTAGGAGCTGGAGGTGCGCTAC 720
Db      661  |||||TCTGTTGTGACCTCTCGAAGAGCAGATAGCCCACTTCTAGGAGCTGGAGGTGCGCTAC 720
Qy      721  |||||TACCATGGGTATTCCTGATCTGCGGAGATGACAGTGGAAACAGATGACAGTGTGACAC 780
Db      721  |||||TACCATGGGTATTCCTGATCTGCGGAGATGACAGTGGAAACAGATGACAGTGTGACAC 780
Qy      781  |||||CCAAACAGCAACAGGCCGAGAAACAGTGCAGTACCCACTGCTGACACAAAGGCCAACAC 840
Db      781  |||||CCAAACAGCAACAGGCCGAGAAACAGTGCAGTACCCACTGCTGACACAAAGGCCAACAC 840
Qy      841  |||||GGACCCCTGTTGGGCAACCAAGAGGGGGCCGAGACCTCATAGGCCAAGAAAGAAACA 900
Db      841  |||||GGACCCCTGTTGGGCAACCAAGAGGGGGCCGAGACCTCATAGGCCAAGAAAGAAACA 900
Qy      901  |||||AAATGAGATGAGGCTAGTGTGACACACTGCGAGTAAATACGACTCTTTGATTAAGTA 960
Db      901  |||||AAATGAGATGAGGCTAGTGTGACACACTGCGAGTAAATACGACTCTTTGATTAAGTA 960
Qy      961  |||||AGTATCTACTCAGGGGTACCTCCAGTGGATGAAAAAGTGTTCGCCCGAACCATGACT 1020
Db      961  |||||AGTATCTACTCAGGGGTACCTCCAGTGGATGAAAAAGTGTTCGCCCGAACCATGACT 1020
Qy      1021  |||||TTAGGACTCTTCAAGTTCCTTTAGAGCATCTCGCAGACCTTGTGCTCAACGGGCAAG 1080
Db      1021  |||||TTAGGACTCTTCAAGTTCCTTTAGAGCATCTCGCAGACCTTGTGCTCAACGGGCAAG 1080
Qy      1081  |||||GAGAAATATTTAAATGCTCCGCTGATGGAGAGTAAATATAGATTGATTTTTCCTT 1140
Db      1081  |||||GAGAAATATTTAAATGCTCCGCTGATGGAGAGTAAATATAGATTGATTTTTCCTT 1140
Qy      1141  |||||GCTGTCATCTACTTGTCTGGAATGCTTAATGTTTCTGTAGACAAACACAGATAAG 1200
Db      1141  |||||GCTGTCATCTACTTGTCTGGAATGCTTAATGTTTCTGTAGACAAACACAGATAAG 1200
Qy      1201  |||||CTATGATCTTTATTAGAG 1218
Db      1201  |||||CTATGATCTTTATTAGAG 1218

RESULT 8
ACAA60455
ID      ACAA60455 standard; cDNA; 1218 BP.
AC      ACAA60455;
AC      ACAA60455;
DT      11-JUN-2003 (first entry)
XX      Novel human secreted and transmembrane protein PRO444 cDNA.
XX      Human; secreted and transmembrane polypeptide; PRO.
XX      fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
XX      PRO1411; PRO10096; PRO3046; PRO307; FGR-3; FGR-4; FGR-1;
XX      FGR-2; PRO6004; PRO356; PRO2630; PRO265; PRO51; bioactive molecule;
XX      toxin; radiolabel; antibody; cell death; chromosome mapping;
XX      gene mapping; transgenic animal; knockout animal; gene therapy;
XX      tissue typing; gene; ss.

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Qy	6	AAAGAGTCGGCCGCGCCGCGCCGCGCCCTCCCTCCGAGTGGAGCCGGAGAGTAAAGT	120
Db	61	AAAGAGTCGGCCGCGCCGCGCCGCGCCCTCCCTCCGAGTGGAGCCGGAGAGTAAAGT	120
Qy	121	CAAGTCCACAGCCCGACCGCGCTGCTTGAGCCCTTGAGGCACGCGAAACGGAGGAGTCT	180
Db	121	CAAGTCCACAGCCCGACCGCGCTGCTTGAGCCCTTGAGGCACGCGAAACGGAGGAGTCT	180
Qy	181	GAGGATTGGAGGACGTCTGTGAGAGGAGAGGAGACAGCGCTCGAGCCTGGAGCGAGCGAGC	240
Db	181	GAGGATTGGAGGACGTCTGTGAGAGGAGAGGAGACAGCGCTCGAGCCTGGAGCGAGCGAGC	240
Qy	241	GGACTGGGGCCCGGGGTAGGCTCTGGAAGAGGCGCGGAGAGAGGTGGGTGGTCAAGC	300
Db	241	GGACTGGGGCCCGGGGTAGGCTCTGGAAGAGGCGCGGAGAGAGGTGGGTGGTCAAGC	300
Qy	301	CTGAGAAACAGCCGAGAGGTTTTCACCGAGGCCCGCGCTTGAGGATCTGAAAGGTTG	360
Db	301	CTGAGAAACAGCCGAGAGGTTTTCACCGAGGCCCGCGCTTGAGGATCTGAAAGGTTG	360
Qy	361	CTAAGAAAGGAGTGTCCCTCTTTCCGAGGCTCTCAACAGAAAGAGTCTTGGGGTGGC	420
Db	361	CTAAGAAAGGAGTGTCCCTCTTTCCGAGGCTCTCAACAGAAAGAGTCTTGGGGTGGC	420
Qy	421	CTTTTGAGAGGCTCGGGCTTAACAGGGGCCAAGATCGCATTTGATTCGAAGTCCCT	480
Db	421	CTTTTGAGAGGCTCGGGCTTAACAGGGGCCAAGATCGCATTTGATTCGAAGTCCCT	480
Qy	481	GTAAGTATATATGTTGGAAATAAGCTCTGCAACTTCTCTTGGCATTCAGTGTGTTAAAC	540
Db	481	GTAAGTATATATGTTGGAAATAAGCTCTGCAACTTCTCTTGGCATTCAGTGTGTTAAAC	540
Qy	541	AAATAGGATGCAAAATTCCTCACTCCAGGTTTATGAAACAGTACTGTGAAATCTGAAAC	600
Db	541	AAATAGGATGCAAAATTCCTCACTCCAGGTTTATGAAACAGTACTGTGAAATCTGAAAC	600
Qy	601	TACCTAAATATGTCCTTTGGTTGGCGGTCTTTCAGGAGCAAGACCTTGGCAAGG	660
Db	601	TACCTAAATATGTCCTTTGGTTGGCGGTCTTTCAGGAGCAAGACCTTGGCAAGG	660
Qy	661	TCTGTTTGTACTCTCGAAGAGCAATAGCCCACTCTTAAGGACTGAGGGTGGCTAC	720
Db	661	TCTGTTTGTACTCTCGAAGAGCAATAGCCCACTCTTAAGGACTGAGGGTGGCTAC	720
Qy	721	TACCATGAGTAATTCCTGTATCTGCCGAGATATACAGTGGAAACATATGACGTGTGAC	780
Db	721	TACCATGAGTAATTCCTGTATCTGCCGAGATATACAGTGGAAACATATGACGTGTGAC	780
Qy	781	CCAACAGCAACAGGCCGAGAAACAGTGCAGTACCCACTGCTGACCAAGAGCCACACAG	840
Db	781	CCAACAGCAACAGGCCGAGAAACAGTGCAGTACCCACTGCTGACCAAGAGCCACACAG	840
Qy	841	GGAACCCGTTCGGCCCAACAGAGAGGGGCCGAGAGCTTATAGCCACAGAAAGAAACA	900
Db	841	GGAACCCGTTCGGCCCAACAGAGAGGGGCCGAGAGCTTATAGCCACAGAAAGAAACA	900
Qy	901	AAATGTGAGAGGGCTAGTGTGGAACACTGCGAGTAATAGGACTCTTGTAGTAAATA	960
Db	901	AAATGTGAGAGGGCTAGTGTGGAACACTGCGAGTAATAGGACTCTTGTAGTAAATA	960
Qy	961	AGTATCTGACTCAGGTCACCTTCAAGTGAATGAAGAAATGTCTTCGCCGGAACCATGACT	1020
Db	961	AGTATCTGACTCAGGTCACCTTCAAGTGAATGAAGAAATGTCTTCGCCGGAACCATGACT	1020
Qy	1021	TTAGGACTCCTTCAAGTCTTATAGACATATCAGCAAGCTTGTGTCTCACAGGCAAG	1080
Db	1021	TTAGGACTCCTTCAAGTCTTATAGACATATCAGCAAGCTTGTGTCTCACAGGCAAG	1080
Qy	1081	GAGAAATTTTAAATGTCTCGCTGATGAGGCAAGATTAATGATTAAGATTGATTTTTCCT	1140
Db	1081	GAGAAATTTTAAATGTCTCGCTGATGAGGCAAGATTAATGATTAAGATTGATTTTTCCT	1140

QY	1141	GCCTGATCTTATTTGTGTGGAATGCTTAATGTTCTGTGACGAAAACAGATTAAG	1200
Db	1141	GCCTGATCTTATTTGTGTGGAATGCTTAATGTTCTGTGACGAAAACAGATTAAG	1200
QY	1201	CTATGATCTTTATTATGAG	1218
Db	1201	CTATGATCTTTATTATGAG	1218
RESULT 10			
ID	ACA65586	standard, cDNA, 1218 BP.	
XX	ACA65586;		
XX	19-JUN-2003	(first entry)	
DE	Human cDNA encoding secreted/transmembrane protein PRO44.		
XX	Human; seg: gene; secreted protein; transmembrane protein; PRO;		
XX	genetic disorder; gene therapy.		
XX	Homo sapiens.		
XX	US2003032057-A1.		
XX	13-FEB-2003.		
XX	15-NOV-2001.	2001US-00002796.	
XX	26-AUG-1997;	97US-0056974P.	
PR	17-SEP-1997;	97US-0059115P.	
PR	18-SEP-1997;	97US-0059263P.	
PR	19-SEP-1997;	97US-0059588P.	
PR	17-OCT-1997;	97US-0062285P.	
PR	24-OCT-1997;	97US-0062816P.	
PR	24-OCT-1997;	97US-0063082P.	
PR	27-OCT-1997;	97US-0063322P.	
PR	29-OCT-1997;	97US-0063733P.	
PR	21-NOV-1997;	97US-0066364P.	
PR	25-NOV-1997;	97US-0066840P.	
PR	16-DEC-1997;	97US-0069694P.	
PR	09-FEB-1998;	98US-0074086P.	
PR	05-FEB-1998;	98US-0074092P.	
PR	25-MAR-1998;	98US-0075294P.	
PR	08-APR-1998;	98US-0081042P.	
PR	14-JUL-1998;	98WO-US014552.	
PR	10-AUG-1998;	98US-009598P.	
PR	18-AUG-1998;	98US-0097000P.	
PR	09-SEP-1998;	98US-0099601P.	
PR	10-SEP-1998;	98US-0099803P.	
PR	10-SEP-1998;	98US-0099811P.	
PR	10-SEP-1998;	98US-0099832P.	
PR	10-SEP-1998;	98WO-US018824.	
PR	14-SEP-1998;	98WO-US019093.	
PR	16-SEP-1998;	98WO-US019330.	
PR	17-SEP-1998;	98US-0100858P.	
PR	17-SEP-1998;	98WO-US019437.	
PR	24-SEP-1998;	98US-0101922P.	
PR	28-OCT-1998;	98US-0106032P.	
PR	20-NOV-1998;	98US-0109306P.	
PR	20-NOV-1998;	98WO-US024855.	
PR	25-NOV-1998;	98WO-US025190.	
PR	01-DEC-1998;	98WO-US025108.	
PR	08-MAR-1999;	99WO-US005028.	
PR	23-MAR-1999;	99US-0125778P.	
PR	02-JUN-1999;	99WO-US012522.	
PR	15-JUN-1999;	99US-0139695P.	
PR	20-JUL-1999;	99US-0145070P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	17-AUG-1999;	99US-0149396P.	
PR	01-SEP-1999;	99WO-US020111.	
PR	08-SEP-1999;	99WO-US020594.	

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028655.
PR 07-DEC-1999; 99US-0169485P.
PR 20-DEC-1999; 99WO-US030959.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US000431.
PR 18-FEB-2000; 2000WO-US000414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 23-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014841.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US017443.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Borstein DA, Desnoyers L, Eaton DJ;
PI Ferrara N, Fong S, Gao W, Gerder H, Gertlisen ME, Goddard A;
PI Godowski PJ, Gurney AJ, Kljavin J, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX WPI: 2003-341960/32.
DR P-FSDB; ABU79780.

XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 3; 255pp; English.

XX The invention relates to an isolated, secreted/transmembrane polypeptide,
CC termed PRO polypeptide, having at least 80% sequence identity to a
CC sequence selected from any one of the 37 sequences appearing as ABU79779
CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
CC under any one of the ATCC numbers given in the specification. Also
CC included are an isolated nucleic acid molecule having at least 80%
CC sequence identity to a sequence selected from any one of the 37 cDNA
CC sequences defined in the specification (or encoding the mature PRO
CC protein or a PRO protein extracellular domain), a PRO expression vector,
CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
CC antibodies and a method for linking a bioactive molecule to a cell
CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
CC radiolabel or an antibody and causes the death of the cell. PRO or the
CC antibody is useful for modulating at least one biological activity of
CC cell expressing the above polypeptides. PRO is useful for identifying
CC agonists or antagonists of PRO, for preparing a variant of PRO, as
CC molecular weight markers for protein electrophoresis purpose and PRO
CC nucleic acid is useful for recombinantly expressing those markers. PRO is
CC also useful as therapeutic agent. PRO is useful in assays to identify
CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probe, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and

CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence encodes a PRO polypeptide

XX Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 8; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCGCGCGTGGCCCTGCGTCATCTTTCCTTCGAGCTGTCA 60
DB 1 CCCACGCGTCCGCGCGCGTGGCCCTGCGTCATCTTTCCTTCGAGCTGTCA 60
QY 61 AAGAGTGGCG 120
DB 61 AAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 CAGTCCACAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CAGTCCACAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GAGGTTGGGACGCTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GAGGTTGGGACGCTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 GGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 GGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 CTGAGAAACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 CTGAGAAACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 CTGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 CTGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 CTTCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 CTTCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 GATAGTGAATGTTGGGAAATAGCTGCGCACTTCTTGCACTGATTTAA 540
DB 481 GATAGTGAATGTTGGGAAATAGCTGCGCACTTCTTGCACTGATTTAA 540
QY 541 AATAGAGTGAATTTCTCAACTCCAGGTTATGAAACAGTACTTGGAAAC 600
DB 541 AATAGAGTGAATTTCTCAACTCCAGGTTATGAAACAGTACTTGGAAAC 600
QY 601 TACCTAAATGATGCTTTGGTGGCGCGTGTCTTGAAGACAGAGCTGG 660
DB 601 TACCTAAATGATGCTTTGGTGGCGCGTGTCTTGAAGACAGAGCTGG 660
QY 661 TCTGTTGTTGACCTCTGAAAGAGACATAGCCACTTCTTAGAGAGTGC 720
DB 661 TCTGTTGTTGACCTCTGAAAGAGACATAGCCACTTCTTAGAGAGTGC 720
QY 721 TACCAATGGGTAATTTCTGTATCTGCGCAATGACATGAAAGATGATG 780
DB 721 TACCAATGGGTAATTTCTGTATCTGCGCAATGACATGAAAGATGATG 780
QY 781 CCAACAGCAACAGCGGAGAGAGAGTACATACCACTGCTGACACAGAGCA 840
DB 781 CCAACAGCAACAGCGGAGAGAGAGTACATACCACTGCTGACACAGAGCA 840

Db 781 CCAACAGCAACAGCCGAGACAGTACCACTGCTGACACAGAGCCAAACACG 840
 Qy 841 GGAACCTGTCGGCCACCAAGAGGGGCGAGAGCTCTATGAGCCAGAGAAACAA 900
 Db 841 GGAACCTGTCGGCCACCAAGAGGGGCGAGAGCTCTATGAGCCAGAGAAACAA 900
 Qy 901 AATATGATGAGGCTAGTGTGAGACACACTGCGAGTAATACGACTCTTTGATAGTA 960
 Db 901 AATATGATGAGGCTAGTGTGAGACACACTGCGAGTAATACGACTCTTTGATAGTA 960
 Qy 961 AATATGATGAGGCTAGTGTGAGACACACTGCGAGTAATACGACTCTTTGATAGTA 1020
 Db 961 AATATGATGAGGCTAGTGTGAGACACACTGCGAGTAATACGACTCTTTGATAGTA 1020
 Qy 1021 TTAGAGCTCCTTCAGTTCCTTTAGAGACATACCTGCGAACCTTGTGCTACAGGGCAAAG 1080
 Db 1021 TTAGAGCTCCTTCAGTTCCTTTAGAGACATACCTGCGAACCTTGTGCTACAGGGCAAAG 1080
 Qy 1081 GAGAAATATTTTATGCTCGCGCTGATGAGAGTAATGATTTGATTTGCTT 1140
 Db 1081 GAGAAATATTTTATGCTCGCGCTGATGAGAGTAATGATTTGATTTGCTT 1140
 Qy 1141 GCTGCTATCTACTTGTCTGGAATGTCTAAATGTTTCTGTAGCAAGAAACAGATAAG 1200
 Db 1141 GCTGCTATCTACTTGTCTGGAATGTCTAAATGTTTCTGTAGCAAGAAACAGATAAG 1200
 Qy 1201 CTATGATCTTTATTAAG 1218
 Db 1201 CTATGATCTTTATTAAG 1218
 Qy 1201 CTATGATCTTTATTAAG 1218
 Db 1201 CTATGATCTTTATTAAG 1218
 RESULT 11
 ACD68242
 ID ACD68242 standard; cDNA; 1218 BP.
 XX
 AC ACD68242;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444 cDNA.
 XX
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemia;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis; gene; ss.
 KM
 OS Homo sapiens.
 PN US2003073130-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 11-DEC-2001; 2001US-00015869.
 XX
 PR 01-SEP-1998; 98US-0098716P.
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PR 10-SEP-1998; 98US-0099741P.
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 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
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 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102310P.
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 PR 30-SEP-1998; 98US-0102484P.
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 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103359P.
 PR 07-OCT-1998; 98US-0103369P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
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 PR 20-OCT-1998; 98US-0105002P.
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 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.

Db 781 CCAACGACCAAGGCGGAGAACAGTCACTGCTGACACAGAGCCACACG 840
Qy 841 GGACCTGTTGGCCACCAAGAGGGGCGAGAGCTCATGAGCCAGAGAAACAA 900
Db 841 GGACCTGTTGGCCACCAAGAGGGGCGAGAGCTCATGAGCCAGAGAAACAA 900
Qy 901 AATATGATGGGCTAGTGTGACACACTGGAGATGAACGAGCTCTGTAGTAAGA 960
Db 901 AATATGATGGGCTAGTGTGACACACTGGAGATGAACGAGCTCTGTAGTAAGA 960
Qy 961 AGTATCTGACTCAACGCTCACTCCAGTGAATGAAAGTCTTCCGCGGAAACATGACT 1020
Db 961 AGTATCTGACTCAACGCTCACTCCAGTGAATGAAAGTCTTCCGCGGAAACATGACT 1020
Qy 1021 TTGAGACTCCTTCAAGTTCCTTTAGACATACCTGCGCAACCTTGCTGACAGGCGCAAG 1080
Db 1021 TTGAGACTCCTTCAAGTTCCTTTAGACATACCTGCGCAACCTTGCTGACAGGCGCAAG 1080
Qy 1081 GAGATATTTTAAATGCTCCGCTGATGACAGATGAATGAATTTGATTTTGTCTT 1140
Db 1081 GAGATATTTTAAATGCTCCGCTGATGACAGATGAATGAATTTGATTTTGTCTT 1140
Qy 1141 GCTGTATCTACTTGTGTGGAATGTCTAAATGTTTCTGTAGCAAAACAGATTAAG 1200
Db 1141 GCTGTATCTACTTGTGTGGAATGTCTAAATGTTTCTGTAGCAAAACAGATTAAG 1200
Qy 1201 CTATGATCTTTATTAAG 1218
Db 1201 CTATGATCTTTATTAAG 1218

RESULT 12

ADA47180
ADA47180 standard; cDNA; 1218 BP.

XX
AC ADA47180;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO444 cDNA.
XX
XX human; ss; gene; secreted protein; transmembrane protein; PRO;
XX
XX VEGF inhibitor; vascular endothelial growth factor;
XX
XX endothelial cell proliferation; T-lymphocyte proliferation;
XX
XX pancreatic beta cell differentiation; chondrocyte proliferation;
XX
XX glucose uptake; free fatty acid; FFA uptake; tissue typing.
OS Homo sapiens.
XX
PN US2003044844-A1.
XX
PD 06-MAR-2003.
XX
PF 01-FEB-2002; 2002US-00066211.
XX
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 16-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0066949P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.

PR 10-AUG-1998; 98US-0059398P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0096601P.
PR 10-SEP-1998; 98US-0096803P.
PR 10-SEP-1998; 98US-0096811P.
PR 10-SEP-1998; 98US-0096812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100688P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101942P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145638P.
PR 17-AUG-1999; 99US-0149336P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US021547.
PR 01-DEC-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028301.
PR 07-DEC-1999; 99US-0164989P.
PR 20-DEC-1999; 99WO-US030099.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019892.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Deenoyers L, Eaton DL,
XX
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
XX
XX Godowski PJ, Gurney AJ, Kijavlin IU, Mather JP, Napier MA, Pan J,
XX
XX Paoni NF, Roy MA, Stewart RA, Tumas D, Watanabe CK, Williams PM,
XX
XX Wood WI, Zhang Z;
XX
XX WPI: 2003-615775/58.
XX
XX P-PDSB; ADA47181.
XX
XX Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
XX
XX inducing redifferentiation and/or proliferation of chondrocytes, and for
XX
XX modulating glucose or free fatty acid uptake by skeletal muscle cells.

XX Claim 1, Fig 4; 254bp; English.
 CC The invention relates to an isolated secreted/transmembrane PRO
 CC polypeptide. The polypeptide and its nucleic acid is useful as an
 CC inhibitor of vascular endothelial growth factor stimulated proliferation
 CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
 CC pancreatic beta cell precursors into mature cell, for induction of
 CC redifferentiation and/or proliferation of chondrocytes and for modulating
 CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
 CC polypeptide and its nucleic acid is useful for generating transgenic or
 CC knock-out animals, for tissue typing and for chromosome identification.
 CC The polypeptide is useful in a number of functional biological assays, as
 CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation PRO polypeptides. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a cDNA encoding a
 CC human secreted/transmembrane PRO polypeptide.
 SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1218; DB 8; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCACGGGCTCGGCGCGCGCTGCGCTCCATCTTCCGCTTCTCTGCAACCTGTGACA 60
 DB 1 CCCACGGGCTCGGCGCGCGCTGCGCTCCATCTTCCGCTTCTCTGCAACCTGTGACA 60
 QY 61 AAGAGTCG 120
 DB 61 AAGAGTCG 120
 QY 121 CAGTGCACACGCCG 180
 DB 121 CAGTGCACACGCCG 180
 QY 181 GAGGCTTGGGAGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 DB 181 GAGGCTTGGGAGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 QY 241 GAGCTGGGCG 300
 DB 241 GAGCTGGGCG 300
 QY 301 CTGAGAAACAGCCGAGAGGTTTCCACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 DB 301 CTGAGAAACAGCCGAGAGGTTTCCACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 361 CTAGAGAGGCGGTTCCCTCTTTGGGGGCTCTCAGCAGAGAGAGGTTCTTGGGGGTCGCC 420
 DB 361 CTAGAGAGGCGGTTCCCTCTTTGGGGGCTCTCAGCAGAGAGAGGTTCTTGGGGGTCGCC 420
 QY 421 CTTCTGAGAGGCTCGCGCTTAACAGAGGCGCGAGAGCTGCATTTGATGTCAGAAATCCCT 480
 DB 421 CTTCTGAGAGGCTCGCGCTTAACAGAGGCGCGAGAGCTGCATTTGATGTCAGAAATCCCT 480
 QY 481 GTAGTGAATGTTGGGAAATAGCTGCAACTTTCTTTGGCAATTCAGTTGTTAAATAC 540
 DB 481 GTAGTGAATGTTGGGAAATAGCTGCAACTTTCTTTGGCAATTCAGTTGTTAAATAC 540
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 DB 541 AATAGATGCAATTTCTCACTCAGGTTATGAAAACAGTACTTGGAAAACGTAAGAAC 600
 QY 601 TACCTAATGATCGCTTGTGGGCGGTGTTCTTACGAGAGGAAACCTTGGCGAGG 660

DB 601 TACCTAATGATCGCTTGTGGGCGGTGTTCTTACGAGAGGAAACCTTGGCGAGG 660
 QY 661 TCTGTTGTGACTCTCCGAGAGGACATAGCCCACTTCTGAGGAGTGGCGGCTAC 720
 DB 661 TCTGTTGTGACTCTCCGAGAGGACATAGCCCACTTCTGAGGAGTGGCGGCTAC 720
 QY 721 TACCATGGGTAATTCCTTATCTGCGGAGATGACATGGAACAGATGACAGTGTGACAC 780
 DB 721 TACCATGGGTAATTCCTTATCTGCGGAGATGACATGGAACAGATGACAGTGTGACAC 780
 QY 781 CCAAGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 781 CCAAGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 841 GGAACCTGTTGGCG 900
 DB 841 GGAACCTGTTGGCG 900
 QY 901 AATGTGATGGGCTAGTGTGAGACACCTGCGAGTATACGAGCTCTTGTAGTAAGTA 960
 DB 901 AATGTGATGGGCTAGTGTGAGACACCTGCGAGTATACGAGCTCTTGTAGTAAGTA 960
 QY 961 AGTATCTGACTGACGCTGACCTCCAGTGGAGTGAATGAAATGTTGCGCGGAGACATGACT 1020
 DB 961 AGTATCTGACTGACGCTGACCTCCAGTGGAGTGAATGAAATGTTGCGCGGAGACATGACT 1020
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 DB 1021 TTAGGACTCTCTCACTTCTTATGAGACATPACTCGCGAAGCTTGTGCTCAACGCGCAAG 1080
 QY 1081 GAGATATTTTAAAGCTCGCGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 DB 1081 GAGATATTTTAAAGCTCGCGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 QY 1141 GCTGTATCTACTTGTCTGAGAAATGTCTAAATGTTTCTGAGCAGAAACACGATTAAG 1200
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 QY 1201 CTATGATCTTTATTAGAG 1218
 DB 1201 CTATGATCTTTATTAGAG 1218
 RESULT 13
 ACH04344
 ID ACH04344 standard; cDNA; 1218 BP.
 XX ACH04344;
 AC
 DT 01-OCT-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO444.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnary;
 KW cardiac; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003044841-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 06-DEC-2001; 2001US-0006856.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.

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 PR 01-SEP-1998; 98US-0098750P.
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 PR 17-SEP-1998; 98US-0100919P.
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 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
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and is derived by analysis of the total score distribution.

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19	483.2	39.7	725	6	BD099384	BD099384 Novel gen
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ALIGNMENTS

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DEFINITION Sequence 8 from Patent WO0077037.
ACCESSION AX403653
VERSION AX403653.1 GI:21437113
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Desnovers, L., Eaton, D.L.,
Farrar, N., Fong, S., Gao, W.Q., Geier, H., Gerlt, M.B.,
Goddard, A., Godowski, P., Gurney, A., Kijavini, I.U., Mather, J.,

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ACCESSION	AX450898			
VERSION				
KEYWORDS				
SOURCE	AX450898.1	GI:22323786		
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurey,A.L., Hillan,K.J., Masters,S.A., Pan,J., Pooni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.			
JOURNAL	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis Patent: WO 0200690-A 5 03-JAN-2002; Genentech, Inc. (US)			
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 ACCESSION AX696937
 VERSION AX696937.1 GI:29497951
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 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 Ferrariz, N., Stewart, T.A., Williams, P.M., Baker, K.P., Denoyers, L.,
 Eaton, D.L., Gao, W.Q., Fan, J., Borstein, D., Fong, S., Goddard, A.,
 Goddard, P.J., Garney, A.L., Smith, V., Tumas, D., Wood, W.L.,
 Grimaldi, C.J., Hillan, K.J., Pao, N.F., Roy, M.A. and Watanabe, C.K.
 Secreted and transmembrane polypeptides and nucleic acids encoding
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 Genentech Inc. (US)

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ORIGIN

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ACCESSION
VERSION
KEYWORDS
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AUTHORS
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
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Xie,M.H., Yamsu,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatic Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
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Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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LOCUS	AC009090	198253 bp	DNA	linear	PRI 19-MAR-2003			
DEFINITION	Human sapiens chromosome 16 clone RP11-407G23, complete sequence.							
ACCESSION	AC009090							
VERSION	AC009090.12	GI:29124043						
KEYWORDS	HTG.							
SOURCE	Human sapiens							
ORGANISM	Human sapiens (human)							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1 (bases 1 to 198253)							
TITLE	DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.							
JOURNAL	Direct Submission							
REFERENCE	2 (bases 1 to 198253)							
AUTHORS	DOE Joint Genome Institute.							
TITLE	Direct Submission							
JOURNAL	Submitted (04-APR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA							
REFERENCE	3 (bases 1 to 198253)							
AUTHORS	DOE Joint Genome Institute.							
TITLE	Direct Submission							
JOURNAL	Submitted (17-DEC-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA							
REFERENCE	4 (bases 1 to 198253)							
AUTHORS	DOE Joint Genome Institute.							
TITLE	Direct Submission							
JOURNAL	Submitted (19-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA							
COMMENT	On Mar 19, 2003 this sequence version replaced gi:27151360. Draft Sequence Produced by DOE Joint Genome Institute							
	www.jgi.doe.gov							
	Finishing completed at Stanford Human Genome Center and Los Alamos National Laboratory							
	www.sshgc.stanford.edu							
	Quality: Phrap Quality >=40 100% of Sequence;							
	Estimated total Number of Errors is 0.							
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source								
ORIGIN								
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Best local Similarity	100.0%; Pred. No. 2e-178;							
Matches	768; Conservative 0; Mismatches 0; Indels 0; Gaps 0							
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D	b			5976	AGAACTGCCATTGGATGTCACGAATCCCGTAGTTGTATAAATGGTGGCAATTAAGCTTGCG	5901
Oy				511	AACCTTCCTTTGGCATTCAGTTGTTAAAAACAATTAGAATGC AAATTCCTC CACTCCAGGT	570
D	b			59016	AACCTTCCTTTGGCATTCAGTTGTTAAAACAAATAGAATGC AATTCCTC CAATCCAGGT	5895
Oy				571	TATGAAAACGTC ACTTGG AAAA CTGAAA AC TACC TA ATGAT GAT CGT CTC TT GT GG GC CG GT	630
D	b			58956	TATGAAAACGTC ACTTGG AAAA CTGAAA AC TACC TA ATGAT GAT CGT CTC TT GT GG GC CG GT	5889
Oy				631	GTTCTTAGCAGCAGAAAG CCTTG GCCA AGGT CTGT GTT TGACT TC TC GAAG ACA CAT TAG C	650
D	b			58896	GTTCTTAGCAGCAGAAAG CCTTG GCCA AGGT CTGT GTT TGACT TC TC GAAG ACA CAT TAG C	5883
Oy				691	CCACTTCCTTAGGGA CTGGAAGGTG CCCTACT ACCATG GGGAATTC CTGAT CTGCCCAGA	750
D	b			58836	CCACTTCCTTAGGGA CTGGAAGGTG CCCTACT ACCATG GGGAATTC CTGAT CTGCCCAGA	5877
Oy				751	TGACAGTGG AACATG ATGAC AGT GTT GA CAC CCAACAGCAA CAGG CCGAGAACAGTSCAGT	810
D	b			58776	TGACAGTGG AACATG ATGAC AGT GTT GA CAC CCAACAGCAA CAGG CCGAGAACAGTSCAGT	5871
Oy				811	ACCCACTGCTGACACAAAGAGCCCA CCA CGSGAACCTG TTCG GGC CACACAAGAGG GGGCGT	870
D	b			58716	ACCCACTGCTGACACAAAGAGCCCA CCA CGSGAACCTG TTCG GGC CACACAAGAGG GGGCGT	5865
Oy				871	AGGACTCATGAGCCAAAGAGAAAACAAAATGTGATG GGC TATG GTTGGACA CACT	930
D	b			58656	AGGACTCATGAGCCAAAGAGAAAACAAAATGTGATG GGC TATG GTTGGACA CACT	5859
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D	b			58596	GGCAGTAATACGCACTCTTTGATATAGTAAGTATCTGAT CTA CGS GCA CTTCCAGTGA	5853
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Oy				1051	CTCGCCCAAGCTTGTGCTCACAGGGC CAAAGAGAA TTTTTAATGCTCCGCTAATGGCAG	1110
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D	b			58356	AATGTTTCTGAGCAGAAAACACGATPAAGCTATGATCTTTATTAGAG	58309
RESULT 7 AX879845						
LOCUS	AX879845	3586 bp	DNA	linear	PAT 17-DEC-2003	
DEFINITION	Sequence 14750 from Patent EP1074617.					
ACCESSION	AX879845					
VERSION	AX879845.1 GI:40034581					
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,U., Ishii,S., Sugiyama,T., Wakematsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: JP 1074617-A 14750 07-FEB-2001; Research Association for Biotechnology (JP) Location/Qualifiers 1..3586 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
AUTHORS						
JOURNAL						
FEATURES						
source						


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Qy      191  GACGCTGTGAGAGGAGGAGAACAGCCGCTGAGCCCTGCGGGCGCGGACCGGACTGCGGC 250
Db      192  GACGCTGTGAGAGGAGGAGAACAGCCGCTGAGCCCTGCGGGCGCGGACCGGACTGCGGC 251
Qy      251  CGGCGGTAGGCTCTGAGAAAGGCGCCCGGAGAGAGGTGGCTGTGCTGAGAACTGAGAAACA 310
Db      252  CGGCGGTAGGCTCTGAGAAAGGCGCCCGGAGAGAGGTGGCTGTGCTGAGAACTGAGAAACA 311
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Db      312  GCCGAGAGGTTTTCCACCGGAGCCCGCGCTTGAGGAGTCTGAAAGAGTTCTTGAAGAGG 371
Qy      371  GGTGCTCCTCTTTCGCGGGGTCTTACCGAAGAGTCTTTCGCGGGTCCGCTCTTGAGAGA 430
Db      372  GTGTCCCTCTTTCGCGGGGTCTTACCGAAGAGTCTTTCGCGGGTCCGCTCTTGAGAGA 431
Qy      431  GGCTGGCGCTAAGAGGCCCA----- 451
Db      432  GGCTGGCGCTAAGAGGCCCAAGGTGAGAGCGACTATCTCTCTGCGGGTGGCTCTTGG 491
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Db      492  TACCGATGAGTCTGACTACTCAGGGGTGCCCGGATAGAAAGGTAGTAGAGGAC 551
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Qy      452  ----- 451
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Qy      466  TGTCCAGATCCCTGTAGTTGATGATGTTGGGATAGCTCTGCAACTTTCTTTGGCAT 525
Db      732  TGTCCAGATCCCTGTAGTTGATGATGTTGGGATAGCTCTGCAACTTTCTTTGGCAT 791
Qy      526  TCAAGTTTAAAAAACAATAGATGATGCAATCTCTCAATCTCAGGTTATGAAAAAGTACT 585
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Qy      766  TGAAGGTGCGGCTACTACTACATGATGATGATGATGATGATGATGATGATGATGATG 825
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Qy 946 TCTGTAGATGA 957
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RESULT 10
AB072745
LOCUS
DEFINITION
AB072745 2453 bp mRNA linear PRI 22-FEB-2003
Macaca fascicularis testis cDNA clone: Qtsa-15931, full insert
sequence.
AB072745
AB072745.1 GI:16041093
oligo capping; fls (full insert sequence).
KEYWORDS
Macaca fascicularis (crab-eating macaque)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.

REFERENCE
AUTHORS
Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Suto, Y.,
Hirai, M., Terao, K., Sugano, S. and Hashimoto, K.
TITLE
Cynomolgus monkey testicular cDNAs for discovery of novel human
genes in the human genome sequence
JOURNAL
BMC Genomics 3 (1), 36 (2002)
12498619
2 (bases 1 to 2453)
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
REFERENCE
AUTHORS
Submitted (09-OCT-2001) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/
Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)

COMMENT

Lab host: TOP10
Vector: pME18S-Fl3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTGTG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo (dt) primer
[ATGTGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-Fl3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method
(Sugano et al., University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing
(5' end primer [CTTGTCTCTTAAAGCTGGC];
3' end primer [CGACCTGACGCTCGAGCAC]).
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/translation="MIVLGAVFLASRLGGLLTLEBHIAHFLGRTAGTATGNSC
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TLLDDEPLPTKDLQKTRITLNLNGEVAQDSDGPKHRTSAVLGLAEKLAGPAS
TGLSPGLELLELQCLKQSHPTWMLFALLKRPATQSEKLTISSSGISDRLVTE
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FEATURES
source

CDS

ORIGIN

EXONESTISGFFAASFWYOCQEFNFGAKPKYPSPWKESTFNDVAFLLAEKILL
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 484 GATGAG 543
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 666 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
 604 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
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 724 AGCAAG 783
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RESULT 11

BC054121

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BC054121 3359 bp mRNA 11neRNA ROD 07-OCT-2003
 Mus musculus RIKEN CDNA 4930470D19 gene, mRNA (CDNA clone MGC:59548
 IMAGE:639310), complete cds.
 BC054121
 BC054121.1 GI:32484165
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 Mus musculus (house mouse)
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 1 (bases 1 to 3359)
 Strausberg, R.L., Fingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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 Carninci, P., Frange, C., Rana, S.S., DeLuca, N.A., Peters, G.J.,
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 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,
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 Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shcherbakov, Y.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherbakov, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Scherach, A., Schein, J.E., Jones, S.J., and Marz, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16895-16903 (2002)
 2388257
 12479932
 2 (bases 1 to 3359)
 Strausberg, R.
 Direct Submission
 Submitted (30-JUN-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Mark Macconochie, Ph.D. and Nancy L. Freeman,
 Ph.D.
 CDNA Library Preparation: Resgen, Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butlerfield,
 Susana Chan, Readman Chin, Chris Fyell, Erin Garland, Ran Guin,
 Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeay, Steven
 Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline
 Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Scott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuydam, Marco Marra.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAX Plate: 109 Row: 9 Column: 12
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ORIGIN

Query Match	49.8%	Score 606	DB 10	Length 3359
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Matches 766; Conservative	0	Mismatches 165	Indels 21	Gaps 4

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QY 71 GCCGCCGCCGCCGCCCTCCTCCGGTGGGCCCGGAGGTAGAGAAAGTCAGTCCACA 130
DB 103 GCCCGTTCGCTGTCCTCCCTCCGGTGGGCCCGAGAGCTAGTCAAAGTCAGTCCACA 162

QY 131 GCCCGACCGCGCTGCTGTAG-----CCCTGGGCAAGCGGAACGGAGGAGTCTGAGGG 185

186 TTGGGACGCTCTGTGAGGAGGGGAAACAGCCGCTGAGCCTGGGGCGGGCGGACCGGACT 245
 223 CTATACGACGAGCTGTAAAGAGAGAGGAGACAGCCGCTGAGCCTGGGGCGGGCGGACCGGACT 282

246 GGAGCCGGGGTAGGCTCTGGAAGAGCCCGGAGAGAGGTGGCCTTGGTTCAGAACTGAG 305

DU 263 GGGGCGGCGCAGGGGCATGGAGAGGGGCGGCTGGTCAAGGCCCTGG 342

QY 306 AAACAGCCGAGAGGTTCACACCGAGGCCGCGCTTGAGGGGATCTGGAGAAGTTCCCTAGA 365

DB 343 AACGACCGGCACACATCTCTCCGAGGCCCGCGCTGGAGGCGCTGAAAGCGGTTCCAG 402

QY 366 AGAGGGTGTTCCTTCTTTGGGGGCTCTACAGAAAGAGTCTTTGGGGTGGCCCTTCT 425

Db 403 AAGAGGGTGTCCCTTTAGGGGACTTGTACTGAAGAGGTCTT --GGGCTACCCCTCCC 460

QY 426 GAGGAGGCTCCGGCTAACAGGGGCCAGACTGCATTGATGTCCAGAAATCCCTGTAGT 485

Db 461 GAGGAGACT-----GGCTAAGAACTGCCAGTGTATGGCCAGCACTCCCACTGGT 509

QY 486 TGATTAATGTTGGGAAATAAGCTCTGCACCTTCTTTGGCACTTCAGTTGTTAAAAACAATA 545

Db 510 TGATTAATCTGGAAATAGCTGCTTACCTTCCTCCAGCACTTCAAGTTGTTAAAAATGATA 569

Qy 546 GGATCCAAATTCTCAACTCCAGGTTATGAAAAAGTACTTGGAAAACCTGAAAACCTACT 605

Db 570 GAATCCAGAGT---TCAGTTCCACATTATGAAAAAGTACTCCGAAAAATTGAAAACTATCT 626

Qy 606 AATATATGTTCTTGGTTGGGCGGTGTTCTTAGCCAGGAGAAAGCCTTGGCCAGGGTCTGT 665

Db 627 AATATATTGTTCTTGGTTGGGCTGTGTGTTCTTAGCAAGCAAGAGCCTTGATCAAGGTTCTGC 686

Qy 666 TGTGTACTCTGAGAGACATATAGCCCACTCTTAAAGGACTGAGAGTCCGGTACTACCA 725

Db 687 TGTCTACTCTTGAGAGACATATAGCCCACTTATGGGAGCTACAGGTGCACTGTACTA 746

Qy 726 TGGGTAAATTCCTGTATCTGCCGAGATGACAGTGGAAACAGATGACAGTGTGACACCCAAC 785

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Qy 786 AACCACAGGCGGAGAACAGTGCAGTACCCATGCTGTACCAAGAGGCCAACACAGGGAAC 845

Db 807 ACCAACAGGCTGGAAPAAAGTACAGTCCCTCATGTCTGATATGTGGAGCCCACTCGGAGAC 866

Qy 846 CTGTTCCGCGCCAAAGAGAGGGGCGAGAGCTCATGAGCCAGAGGAAAGAAACAAATG 905

Db 867 CTGTCCGCGCTCCAAAGAGAGGCGCGAGACCTCATATAGCCAAAGAGAAAGAAACAAATG 926

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Db 927 TGGATGGGTTAGTCTGGACACACTGGCGGTAATACGACTCTTGTAGATTA 978

RESULT 12	
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PRI 26-FEB-2002	

ACCESSION	AB075852
VERSION	AB075852.1
KEYWORDS	GI:18916844
NAME	These samaras (human)

SOURCE
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ORGANISM
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1
AUTHORS
Nagase, T., Kikuno, R. and Ohara, O.
TITLE
Prediction of the coding sequences of unidentified human genes.
XXII. The complete sequences of 50 new cDNA clones which code for

large proteins
DNA Res. 8 (6), 319-327 (2001)
JOURNAL
21842142
MEDLINE
PUBMED 11853319

REFERENCE	2 (bases 1 to 3473)
AUTHORS	Ohara, O., Nagase, T. and Kikuno, R.
TITLE	Direct Submission
JOURNAL	Submitted (06-DEC-2001) Osamu Ohara, Kazusa DNA Research Institute.

Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL: <http://www.kazusa.or.jp/huge>, Tel: 81-438-52-3913, Fax: 81-438-52-3914)

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DEFINITION	AC118500 211897 bp DNA linear HMG 19-NOV-2002
ACCESSION	Rattus norvegicus clone CH230-144P21, WORKING DRAFT SEQUENCE, 6
VERSION	unordered pieces.
KEYWORDS	AC118500 AC118500.4 GI:25073691
SOURCE	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
ORGANISM	Rattus norvegicus (Norway rat)
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	Rattus.
REFERENCE	1 (bases 1 to 211897)
AUTHORS	Muzny,D.Merile., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 211897)

REFERENCE 3 (bases 1 to 211897)

JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:23269807.

Allen, C., Allen, H., Alsbrooks, S., Amlin, A., Anguiano, D.,
Anyalele, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
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Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Sma's, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorreller, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,
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Williams, G., Willison, R., Wlisczyk, R., Wooden, H., Worley, K.,
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Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submissions

Unpublished

2 (bases 1 to 211897)

Worley, R.C.

Direct Submissions

Submitted (18-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 211897)

Rat Genome Sequencing Consortium.

Direct Submissions

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced g1:23269807.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome

[REDACTED]

1

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:15341959.
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarsson, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loussened, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nannavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAP Plate: 26 Row: 1 Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.

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ORIGIN

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Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS BD249821
DEFINITION 33 human secreted proteins.
ACCESSION BD249821
VERSION BD249821.1 GI:33059591
KEYWORDS JP 2002540763-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2133)
Rosen, C.A., Ruben, S.M., Ebner, R., Young, P.E., Ni, J., Soppet, D.R.,
Moore, P.A., Shi, Y., Lafleur, D.W., Olsen, H.S., Florence, K.A. and
Komatsoulis, G.
33 human secreted proteins
Patent: JP 2002540763-A 23 03-DEC-2002;
HUMAN GENOME SCIENCES INC
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PN JP 2002540763-A/23
PD 03-DEC-2002
PF 08-FEB-2000 JP 2000598519
PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN W RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
NI,
PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLUEUR, HENRIK

COMMENT

PI S OLSEN,
PI KIMBERLY A FLORENCE, GEORGE KOMATSOUKIS
PC C12N15/09, A61K31/7115, A61K38/00, A61K48/00, A61P1/00, A61P1/04,
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PC A61P12/06,
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ORIGIN

Query Match 41.5%; Score 505.4; DB 6; Length 2133;
 Best Local Similarity 99.8%; Pred. No. 1e-113;
 Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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